

**Hart, Edward**

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**From:** Swope, Sheridan  
**Sent:** Friday, March 05, 2004 11:16 AM  
**To:** Hart, Edward  
**Subject:** FW: 09/966,880

**Importance:** High

Ed, the applicants have again made changes to the claims that require an additional search for this case (we're negotiating an allowance).

So, would you add the following to my rush search?  
For 09/966,880, Pls search and interference search:

SID 7: full-length and oligo search (20NTs) against the NT data bases.

Thanks in advance for your great service!  
Sheridan

**[Swope, Sheridan]** Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652  
Recombinant Enzymes  
571-272-0943 (voice)  
E03A70 Remsen Bld (Office)  
E03C70 Remsen Bld (Mailbox)

0574  
3/5/04



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 115892**

**TO: Sheridan Swope**  
**Location: REM-3A70**  
**Art Unit: 1652**  
**Friday, March 05, 2004**

**Case Serial Number: 09/966880**

**From: Edward Hart**  
**Location: Biotech-Chem Library**  
**REM-1A55**  
**Phone: 571-272-2512**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Swope,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 21:01:22 ; Search time 2776 Seconds

(without alignments)  
9321.250 Million cell updates/sec

Title: US-09-966-880A-7\_COPY\_80\_676

Perfect score: 597  
Sequence: 1 atgacagcctcttgatga.....ctcgacttggagacttga 597

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 692750

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

GenBdb1:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_on:\*  
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41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	2.5	17	6	BD200908
2	15	2.5	20	6	AR298295
3	14	2.3	17	6	AX728573
4	14	2.3	17	6	AX759439
5	14	2.3	17	6	BD200909
6	14	2.3	20	6	AR026494
7	14	2.3	20	6	AR026495
8	14	2.3	20	6	AX487439
9	13	2.2	17	6	AX333965
10	13	2.2	17	6	AX323966
11	13	2.2	17	6	AX499488
12	13	2.2	17	6	AX499489
13	13	2.2	17	6	AX499490
14	13	2.2	17	6	AX499491
15	13	2.2	17	6	AX499492
16	13	2.2	17	6	AX673539
17	13	2.2	17	6	AX687581
18	13	2.2	17	6	AX687582
19	13	2.2	17	6	AX687583
20	13	2.2	17	6	AX687584
21	13	2.2	17	6	AX687585
22	13	2.2	17	6	AX735945
23	13	2.2	17	6	BD104902
24	13	2.2	19	6	AR241182
25	13	2.2	19	6	AR253259
26	13	2.2	19	6	AX129413
27	13	2.2	19	6	AX129414
28	13	2.2	19	6	AX259857
29	13	2.2	19	6	BD084645
30	13	2.2	20	4	DOCP43801
31	13	2.2	20	6	AR098868
32	13	2.2	20	6	I79708
33	13	2.2	20	6	AR257223
34	13	2.2	20	6	AR337175
35	13	2.2	20	6	AX428287
36	13	2.2	20	6	BD138115
37	12	2.0	13	6	AX358112
38	12	2.0	14	6	I43504
39	12	2.0	15	6	A09427
40	12	2.0	15	6	A10630
41	12	2.0	15	6	A11578
42	12	2.0	15	6	A24554
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44	12	2.0	15	6	A51056
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#### ALIGNMENTS

RESULT 1  
BD200908  
LOCUS  
DEFINITION BD200908 17 bp RNA linear PAT 17-JUL-2003  
Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response.  
ACCESSION BD200908  
VERSION BD200908.1 GI:33010678  
KEYWORDS JP 2002509721-A/3934.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 17)  
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.  
AUTHORS Method and reagent for treating diseases or conditions concerning  
TITLE

JOURNAL molecule participating in vasculogenic response  
 Patent: JP 2002509721-A 3934 02-APR-2002;  
 RIBOZYME PHARMACEUTICALS INC  
 OS Homo sapiens (human)  
 PN JP 2002509721-A/3934  
 PD 02-APR-2002  
 PF 24-MAR-1999 JP 2000541291  
 PR 27-MAR-1998 US 60/079678  
 PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
 PI JAMES A MCSWIGGEN

PC C12N15/00, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
 A61P29/00,  
 PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
 C12N5/00  
 CC Method and reagent for treating diseases or conditions CC  
 CC concerning molecule  
 CC participating in vasculogenic response  
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 FT source 1. .17  
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QY 36 TTACCAATTCAGAAA 50  
 1 TTACCAATTCAGAAA 15

RESULT 2  
 AR298295/c 20 bp DNA linear PAT 12-JUN-2003  
 LOCUS AR298295  
 DEFINITION Sequence 10030 from patent US 6537751.  
 ACCESSION AR298295  
 VERSION AR298295.1 GI:31685579  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.  
 TITLE Biallelic markers for use in constructing a high density  
 disequilibrium map of the human genome  
 JOURNAL Patent: US 6537751-A 10030 25-MAR-2003;  
 FEATURES Location/Qualifiers  
 source 1. .20  
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## ORIGIN

Query Match 2.5%; Score 15; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 GAGGAGTTCTTTA 38  
 15 GAGGAGTTCTTTA 1

RESULT 3  
 AX728573 17 bp DNA linear PAT 08-MAY-2003  
 LOCUS AX728573  
 DEFINITION Sequence 207 from Patent WO03025175.  
 ACCESSION AX728573  
 VERSION AX728573.1 GI:30507916

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
 Telesman, A., Anson, R. and Tuijinder, M.  
 TITLE Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or virus resistance and their use as  
 medicines  
 JOURNAL Patent: WO 03025175-A 207 27-MAR-2003;  
 FEATURES Molecular Engines Laboratories (FR)  
 source 1. .17  
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## ORIGIN

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QY 247 TCCTGAGCCCCCTG 260  
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RESULT 4  
 AX759499 17 bp DNA linear PAT 25-JUN-2003  
 LOCUS AX759499  
 DEFINITION Sequence 2820 from Patent WO03040369.  
 ACCESSION AX759499  
 VERSION AX759499.1 GI:32254115  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
 Telesman, A., Anson, R. and Tuijinder, M.  
 TITLE Sequences involved in tumoral suppression, tumoural reversion,  
 apoptosis and/or viral resistance phenomena and their use as  
 medicines  
 JOURNAL Patent: WO 03040369-A 2820 15-MAY-2003;  
 FEATURES Molecular Engines Laboratories (FR)  
 source 1. .17  
 Location/Qualifiers  
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RESULT 5  
 BD200909 17 bp RNA linear PAT 17-JUN-2003  
 LOCUS BD200909  
 DEFINITION Method and reagent for treating diseases or conditions concerning  
 molecule participating in vasculogenic response.  
 ACCESSION BD200909  
 VERSION BD200909.1 GI:33010679  
 KEYWORDS JP 2002509721-A/3935.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 17)  
Mammalia: Eutheria; Primates; Catarrhini; Homiidae; Homo.  
Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswigen, J.A.  
TITLE Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response  
JOURNAL Patent: JP 2002509721-A 3935 02-Apr-2002;  
RIBOZYME PHARMACEUTICALS, INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002509721-A/3935  
PD 02-APR-2002  
PR 24-MAR-1999 JP 2000541291  
PI 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PI JAMES A MCSWIGEN  
PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00,  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1..17  
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Best Local Similarity 100.0%; Pred. No. 7e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 37 TACCAATTCAAAA 50  
1 TACCAATTCAAAA 14

Db

RESULT 6  
LOCUS AR026494 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1 from patent US 5856099.  
ACCESSION AR026494  
VERSION AR026494.1 GI:5937334  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
Mitsugata, L., Bennett, C., Frank, J., Dean, N. and Geiger, T.  
TITLE Antisense compositions and methods for modulating type I  
interleukin-1 receptor expression  
JOURNAL Patent: US 5856099-A 1 05-JAN-1999;  
FEATURES  
LOCATION/Qualifiers  
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CY 373 GGGCTGGCGGCGCT 386  
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Db

RESULT 7  
LOCUS AR026495

LOCUS AR026495 20 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5856099.  
ACCESSION AR026495  
VERSION AR026495.1 GI:5937335  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
Mitsugata, L., Bennett, C., Frank, J., Dean, N. and Geiger, T.  
TITLE Antisense compositions and methods for modulating type I  
interleukin-1 receptor expression  
JOURNAL Patent: US 5856099-A 2 05-JAN-1999;  
FEATURES  
LOCATION/Qualifiers  
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Db

RESULT 8  
LOCUS AX487439 20 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 4739 from Patent WO02053728.  
ACCESSION AX487439  
VERSION AX487439.1 GI:22321587  
KEYWORDS  
SOURCE Candida albicans  
ORGANISM Candida albicans  
REFERENCE 1  
Roemer, T., Jiang, B., Boone, C., Bussey, H. and Olsen, K.L.  
TITLE Gene disruption methodologies for drug target discovery  
JOURNAL Patent: WO 02053728-A 4739 11-JUL-2002;  
Elitra Pharmaceuticals, Inc. (US)  
FEATURES  
LOCATION/Qualifiers  
source 1..20  
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CY 352 GACCGCAAGGCTGA 365  
14 GACCGCAAGGCTGA 1

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RESULT 9  
LOCUS AX323965 17 bp DNA linear PAT 02-SEP-2002  
DEFINITION Sequence 103 from Patent WO0192512.  
ACCESSION AX323965  
VERSION AX323965.1 GI:18094716  
KEYWORDS  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
REFERENCE 1  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
UNIVERSITY OF DELAWARE (US)  
Patent: WO 0192512-A 103 06-DEC-2001;  
FEATURES  
source  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 16 CGGCGTGAGACCT 4  
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AX323966 17 bp DNA linear PAT 02-SEP-2002  
LOCUS Sequence 104 from Patent WO0192512.  
DEFINITION AX323966  
ACCESSION AX323966  
VERSION AX323966.1 GI:18094717  
KEYWORDS  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE  
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
UNIVERSITY OF DELAWARE (US)  
Patent: WO 0192512-A 104 06-DEC-2001;  
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DB 2 CGGCGTGAGACCT 14  
RESULT 11  
AX499488 17 bp DNA linear PAT 27-SEP-2002  
LOCUS Sequence 795 from Patent EP1229046.  
DEFINITION AX499488  
ACCESSION AX499488  
VERSION AX499488.1 GI:23381781  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 795 07-AUG-2002;  
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 70 CGGCGTGAGACCT 82  
DB 2 CGGCGTGAGACCT 14

AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
UNIVERSITY OF DELAWARE (US)  
Patent: WO 0192512-A 103 06-DEC-2001;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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AX323966 17 bp DNA linear PAT 02-SEP-2002  
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DEFINITION AX323966  
ACCESSION AX323966  
VERSION AX323966.1 GI:18094717  
KEYWORDS  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE  
AUTHORS Kmiec, E.B., Gamper, H.B., Rice, M.C. and Kim, J.  
TITLE Targeted chromosomal genomic alterations in plants using modified  
JOURNAL single stranded oligonucleotides  
UNIVERSITY OF DELAWARE (US)  
Patent: WO 0192512-A 104 06-DEC-2001;  
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DB 2 CGGCGTGAGACCT 14  
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DEFINITION AX499488  
ACCESSION AX499488  
VERSION AX499488.1 GI:23381781  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 795 07-AUG-2002;  
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/mol\_type="unassigned DNA"  
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 2 CGGCGTGAGACCT 14

QY 385 CTGCACCGCGCCG 397  
DB 15 CTGCACCGCGCCG 3

RESULT 14  
LOCUS AX499491/c 17 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 798 from Patent EP1229046.  
ACCESSION AX499491  
VERSION AX499491.1 GI:23381784  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Zhan, J.  
JOURNAL Human testis expressed patched like protein  
Patent: EP 1229046-A 798 07-AUG-2002;  
Neomica, Inc. (US)  
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source location/Qualifiers  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCCG 397  
DB 14 CTGCACCGCGCCG 2

RESULT 15  
LOCUS AX499492/c 17 bp DNA linear PAT 27-SEP-2002  
DEFINITION Sequence 799 from Patent EP1229046.  
ACCESSION AX499492  
VERSION AX499492.1 GI:23381785  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Zhan, J.  
JOURNAL Human testis expressed patched like protein  
Patent: EP 1229046-A 799 07-AUG-2002;  
Neomica, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCCG 397  
DB 13 CTGCACCGCGCCG 1

RESULT 16  
LOCUS AX673599 17 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 2044 from Patent WO03004526.

ACCESSION AX673599  
VERSION AX673599.1 GI:29331947  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Telerman, A., Anson, R. and Tuijinder, M.  
JOURNAL Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or resistance to viruses and their use as  
medicines  
Patent: WO 03004526-A 2044 16-JAN-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATCCTTTTCACTG 132  
DB 2 ATCCTTTTCACTG 14

RESULT 17  
LOCUS AX687581/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 313 from Patent EP1281758.  
ACCESSION AX687581  
VERSION AX687581.1 GI:29410277  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
mdz12  
Patent: EP 1281758-A 313 05-FEB-2003;  
Neomica, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCCG 258  
DB 17 CTCCTGAGGCCG 5

RESULT 18  
LOCUS AX687582/c 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 314 from Patent EP1281758.  
ACCESSION AX687582  
VERSION AX687582.1 GI:29410278  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 314 05-FEB-2003;  
Neomica, Inc. (US)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGAGAGCCCC 258  
DB 16 CTCCTGAGAGCCCC 4  
RESULT 19  
AX687583 17 bp DNA linear PAT 31-MAR-2003  
LOCUS Sequence 315 from Patent EPI281758.  
DEFINITION AX687583  
ACCESSION AX687583.1 GI:29410279  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 315 05-FEB-2003;  
Neomica, Inc. (US)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGAGAGCCCC 258  
DB 15 CTCCTGAGAGCCCC 3  
RESULT 20  
AX687584 17 bp DNA linear PAT 31-MAR-2003  
LOCUS Sequence 316 from Patent EPI281758.  
DEFINITION AX687584  
ACCESSION AX687584.1 GI:29410280  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 316 05-FEB-2003;  
Neomica, Inc. (US)  
JOURNAL

FEATURES  
source  
Location/Qualifiers  
1. .17  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGAGAGCCCC 258  
DB 14 CTCCTGAGAGCCCC 2  
RESULT 21  
AX687585 17 bp DNA linear PAT 31-MAR-2003  
LOCUS Sequence 317 from Patent EPI281758.  
DEFINITION AX687585  
ACCESSION AX687585.1 GI:29410281  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 317 05-FEB-2003;  
Neomica, Inc. (US)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 2.2%; Score 13; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGAGAGCCCC 258  
DB 13 CTCCTGAGAGCCCC 1  
RESULT 22  
AX735945 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 1535 from Patent WO03025177.  
DEFINITION AX735945  
ACCESSION AX735945.1 GI:30515222  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 Telerman, A., Anson, R. and Thijnder, M.  
AUTHORS Sequences involved in phenomena of tumour suppression, tumour  
TITLE reversion, apoptosis and/or resistance to viruses and the use  
thereof as medicaments  
JOURNAL Patent: WO 03025177-A 1535 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 TCACCTCTCTGAG 254  
 |||||  
 16 TCACCTCTCTGAG 4

RESULT 23  
 BD104902 17 bp DNA linear PAT 27-AUG-2002  
 LOCUS Kit and method for determining HLA type.  
 ACCESSION BD104902  
 VERSION BD104902.1 GI:22650476  
 KEYWORDS WO 0192572-A/1006.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.  
 TITLE Kit and method for determining HLA type  
 JOURNAL Patent: WO 0192572-A 1006 06-DEC-2001;  
 NISSHINO INDUSTRIES INC.,SYSTEM RESEARCH INC.,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA

COMMENT OS Artificial Sequence  
 PN WO 0192572-A/1006  
 PD 06-DEC-2001  
 PF 01-JUN-2001 WO 2001JP004662  
 PR 01-JUN-2000 JP 00P 164798  
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, PI

FEATURES  
 source 1. .17  
 Location/Qualifiers  
 /organism="Artificial Sequence".  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"

ORIGIN  
 Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCACGTGG 172  
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 3 GGCTGCACGTGG 15

RESULT 24  
 AR241182 19 bp DNA linear PAT 20-DEC-2002  
 LOCUS Sequence 9 from patent US 6468983.  
 ACCESSION AR241182  
 VERSION AR241182.1 GI:27286412  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.  
 TITLE Rnae L activators and antisense oligonucleotides effective to treat telomerase-expressing malignancies  
 JOURNAL Patent: US 6468983-A 9 22-OCT-2002;  
 FEATURES Location/Qualifiers

source 1. .19  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 2.2%; Score 13; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407  
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 3 CCGGGGTGCAAT 15

RESULT 25  
 AR253259 19 bp DNA linear PAT 20-DEC-2002  
 LOCUS AR253259/c  
 ACCESSION AR253259  
 VERSION AR253259.1 GI:27301682  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Short,J.M.  
 TITLE Non-stochastic generation of genetic vaccines  
 JOURNAL Patent: US 6479258-A 4 12-NOV-2002;  
 FEATURES Location/Qualifiers  
 source 1. .19  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 2.2%; Score 13; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCTCCCA 520  
 |||||  
 15 GTTCGTCTCCCA 3

RESULT 26  
 AX129413/c 19 bp DNA linear PAT 15-MAY-2001  
 LOCUS AX129413  
 DEFINITION Sequence 631 from Patent WO0130362.  
 ACCESSION AX129413  
 VERSION AX129413.1 GI:14135718  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 TITLE Robbins,J.W. and Tritz,R.  
 JOURNAL Ribozyme therapy for the treatment of proliferative skin and eye diseases  
 PATENT: WO 0130362-A 631 03-MAY-2001;  
 IMMUSOL, INC. (US)  
 FEATURES Location/Qualifiers  
 source 1. .19  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 /note="Cdk5 ribozyme binding site"

ORIGIN  
 Query Match 2.2%; Score 13; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 GCCTGGAGAGGC 493

Db 17 GCCTGGGAAGGC 5

RESULT 27  
AX129414/c 19 bp DNA linear PAT 15-MAY-2001  
DEFINITION Sequence 632 from Patent WO0130362.  
ACCESSION AX129414  
VERSION AX129414.1 GI:14135719  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Robbins,J.M. and Tritz,R.  
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases  
JOURNAL Patent: WO 0130362-A 632 03-MAY-2001;  
IMMUSOL, INC. (US)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="Cdk6 ribozyme binding site"

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 GCCTGGGAAGGC 493  
Db 16 GCCTGGGAAGGC 4

RESULT 28  
AX259857/c 19 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 84 from Patent WO0172822.  
ACCESSION AX259857  
VERSION AX259857.1 GI:1650931  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamailard,M.  
TITLE Genes involved in intestinal inflammatory diseases and use thereof  
JOURNAL Patent: WO 0172822-A 84 04-OCT-2001;  
Fondation Jean Dausset-Ceph (FR)  
FEATURES  
source Location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TCCGCTGGGCTAA 65  
Db 18 TCCGCTGGGCTAA 6

RESULT 29  
BD084645 19 bp DNA linear PAT 27-AUG-2002  
LOCUS BD084645

DEFINITION RNase L activators and antisense oligonucleotides effective to treat telomerase-expressing malignancies.  
ACCESSION BD084645  
VERSION BD084645.1 GI:22630255  
KEYWORDS JP 2001524100-A/9.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.  
TITLE RNase L activators and antisense oligonucleotides effective to treat telomerase-expressing malignancies  
JOURNAL Patent: JP 2001524100-A 9 27-NOV-2001;  
THE CLEVELAND CLINIC FOUNDATION,NATIONAL INSTITUTES OF HEALTH  
COMMENT OS Artificial Sequence  
PN JP 2001524100-A/9  
PD 27-NOV-2001  
PF 13-APR-1998 JP 1998546125  
PR 21-APR-1997 US 60/044507,03-FEB-1998 US 09/018125 PI  
ROBERT H SILVERMAN,SEIJI KONDO,JOHN K COWELL,GUYING LI,PAUL F  
PI TORRENCE  
PC C07H21/00,C07H21/02,C12Q1/68,A61K48/00  
CC Description of Artificial Sequence: oligonucleotide FH Key  
FT source 1..19  
FT Location/Qualifiers  
1..19  
/organism="Artificial Sequence".  
/organism="synthetic construct"  
/mol\_type="Genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGCTGCAAT 407  
Db 3 CCGGGCTGCAAT 15

RESULT 30  
DOGp43801 20 bp DNA linear MM 17-JUN-1996  
LOCUS DOGp43801  
DEFINITION Dog (Clone: CXK.438) primer for STS 438, 5' end.  
ACCESSION L24320  
VERSION L24320.1 GI:402023  
KEYWORDS PCR identification; PCR primer; STS.  
SEGMENT 1 of 2  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.  
TITLE One hundred and one new simple sequence repeat-based markers for the canine genome  
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)  
MEDLINE 95268214  
PUBMED 7749226  
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in pBlueScript+), adult spleen DNA.  
Submitted by: Fred Hutchinson Cancer Research Center  
Transplantation Biology Dept  
1124 Columbia; Mailstop M318  
Seattle, WA 98104, USA  
e-mail: EOstrander@hl.gov  
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)  
PCR Profile: Denaturation: 94 degrees C for 1.00 minute  
Annealing: 55 or 59 degrees C for 0.45 minutes  
Polymerization: 74 degrees C for 1.00 minutes

PCR Cycles: 33  
Final Extension: 74 degrees C for 5.00 minutes

FEATURES	Location/Qualifiers
source	1. .20

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primer_bind      /tissue_11b="B. Ostrander, in pbluescript+"
ORIGIN           1. .20

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Query Match      2.2%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	303	CCCCAACCTCAGT	315
Db	1	CCCCAACCTCAGT	13

RESULT 31			
AR098868			
LOCUS	AR098868	20 bp	DNA
DEFINITION	Sequence 3 from patent US 6077695.		linear
Accession			PAT 14-FEB-2001

```

REFERENCE 1 (bases 1 to 20)
AUTHORS Trofater, J.A., Maccollin, M.M. and Gussella, J.F
TITLE Tumor suppressor meflin and antibodies thereof
JOURNAL Patent: US 6077665-A 3 20-JUN-2000;
FEATURES Location/Qualifiers
SOURCE 1. 20

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Query Match      2.2%   Score 13   DB 6; Length 20
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels
QY      118 ACATCCCTTTTAC 130
      |||||
Db       8 ACATCCCTTTTAC 20

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RESULT 32	LOCUS	20 bp	DNA	linear	PAT 10-UTN-1988
179708	179708	Sequence 3 from patent US 5707865.			
179708	179708				

ORIGIN			
Query Match	2.2%	Score 13;	DB 6; Length 20;
Best Local Similarity	10.0%;	Pred. No.	2.5e+05;

	Matches	13, Conservative	0; Mismatches	0; Indels	0; Gaps	0;
QY	118	ACATCCTTTTCAC	130			
Db	8	ACATCCTTTTCAC	20			

RESULT 33					
AR257223/c					
LOCUS	AR257223	20 bp	DNA		
DEFINITION	Sequence	78	from patent US 6485974.		
ACCESSION	U0357223				
					PAT 20-DEC-2002
					Linear

```

REFERENCE      1 (bases 1 to 20)
AUTHORS      Popoff, I
TITLE      Antisense modulation of PRNP2 expression
JOURNAL      Patent: US 6485974-A 78 26-NOV-2002;
FEATURES
    source
        1..20
        /organism="unknown"
        /mol_type="genomic DNA"
ORIGIN

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QY	108	TCACAGTGTCTACA	120
Db	13	TCACAGTGTCTACA	1

RESULT 34	LOCUS	SEQUENCE	LENGTH	DATE	FILE
AR337175	AR337175	Sequence 100 from patent US 6566135.	20 bp	11-Aug-2003	linear
DEFINITION	AR337175	GI:33723029			
ACCESSION	AR337175				
VERSION	AR337175.1				
KEYWORDS					
SOURCE	Unknown.				

ORIGIN	/mol_type="genomic DNA"
Query Match	2.2%; Score 13; DB 6; Length 20;
Best Local Similarity	100.0%; Pred. No. 2.5e+05;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	447	TACTTTGTAGAA	455
Db	4	TACTTTGTAGAA	16

RESULT	35
AX428287/c	
LOCUS	AX428287 20 bp
DEFINITION	Sequence 9 from Patent WO0233056.
ACCESSION	AX428287
VERSION	AX428287.1 GI:21538245
KEYWORDS	
SOURCE	Homo sapiens (human)
PAT	20-JUN-2002
linear	

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

## REFERENCE

1 Koehler, R.H.  
Regulation of human serine-threonine protein kinase  
JOURNAL  
Patent: WO 0233056-A 9 25-APR-2002;

## FEATURES

source  
1..20  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
/note="PCR primer"

## ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCTCGACTGGGA 206  
|||||  
19 TCTCGACTGGGA 7

RESULT 36  
BD138115/c 20 bp DNA linear PAT 18-SEP-2002

LOCUS BD138115  
DEFINITION Antisense modulation of human MDM2 expression.

ACCESSION BD138115  
VERSION BD138115.1 GI:22233060

KEYWORDS JP 2002508944-A/41.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 20)

AUTHORS Miraglia, L.J., Nepo, P., Graham, M.J., Montia, B.P. and Cowser, L.M.

TITLE Antisense modulation of human MDM2 expression

JOURNAL Patent: JP 2002508944-A 41 26-MAR-2002;

COMMENT ISIS PHARMACEUTICALS INC

OS Unidentified  
PN JP 2002508944-A/41  
PD 26-MAR-2002  
PF 26-MAR-1999 JP 2000538025  
PR 26-MAR-1998 US 09/048610  
PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PI COMSERT

PC C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//

PC C12Q1/68,

PC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Antisense modulation of human MDM2 expression FH Key

Location/Qualifiers

FT source 1..20

1..20 /organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

## RESULT 37

AX358112/c 13 bp DNA linear PAT 13-FEB-2002

## DEFINITION

Sequence 7 from Patent WO0194394.

## ACCESSION

AX358112

## VERSION

AX358112.1 GI:18674859

## KEYWORDS

SOURCE

ORGANISM

Arabisopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

Tilka, J.M., Hood, E.E. and Howard, J.A.

Novel plant promoter sequences and methods of use for same

Patent: WO 0194394-A 7 13-DEC-2001;

ProdiGene, Inc. (US)

Location/Qualifiers

1..13

/organism="Arabisopsis thaliana"

/mol\_type="unassigned DNA"

/db\_xref="taxon:3702"

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Query Match 2.0%; Score 12; DB 6; Length 13;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCCTCCGCTA 191

|||||

13 CTTCCTCCGCTA 2

|||||

RESULT 39

A09427/c 15 bp DNA linear PAT 09-NOV-1993

LOCUS A09427

DEFINITION Oligonucleotide (b3).

ACCESSION A09427

VERSION A09427.1 GI:490532

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

artificial sequences.

```

REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S. and Yamada,H.
TITLE Process for production of somatostatin
JOURNAL Patent: EP 0197558-A 33 15-OCT-1986;
FEATURES FUJISAWA PHARMACEUTICAL CO., LTD
SOURCE Location/Qualifiers
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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4
RESULT 40
LOCUS A10630 15 bp DNA linear PAT 02-DEC-1993
DEFINITION Oligonucleotide (B3).
ACCESSION A10630
VERSION A10630.1 GI:490758
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S., Ono,H. and Kitaguchi,T.
TITLE Process for production of gamma-interferon
JOURNAL Patent: EP 0176916-A 15 09-APR-1986;
FEATURES FUJISAWA PHARMACEUTICAL CO., LTD
SOURCE Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4
RESULT 41
LOCUS A11578 15 bp DNA linear PAT 16-NOV-1993
DEFINITION oligonucleotide 'b3'.
ACCESSION A11578
VERSION A11578.1 GI:491120
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S., Ono,H. and Kitaguchi,T.
TITLE 59 Valine insulin-like growth factor I and process for production thereof
JOURNAL Patent: EP 0158893-A 74 23-OCT-1985;
FEATURES FUJISAWA PHARMACEUTICAL CO., LTD
SOURCE Location/Qualifiers
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/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4
RESULT 42
LOCUS A24554 15 bp DNA linear PAT 24-JAN-1995
DEFINITION PROM38 PCR primer.
ACCESSION A24554
VERSION A24554.1 GI:833371
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS DNA, DNA CONSTRUCTS, CELLS AND PLANTS DERIVED THEREFROM
JOURNAL Patent: WO 9307275-A 5 15-APR-1993;
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGGCC 257
Db 3 CTCCTGGAGGCC 14
RESULT 43
LOCUS A35098 15 bp DNA linear PAT 06-DEC-1996
DEFINITION Synthetic IGF-I gene oligo.
ACCESSION A35098
VERSION A35098.1 GI:1926757
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S. and Kusumoki,C.
TITLE Process for production of insulin-like growth factor I and plasmid for production thereof
JOURNAL Patent: EP 0219814-A 48 29-APR-1987;
FEATURES FUJISAWA PHARMACEUTICAL CO., LTD
SOURCE Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4

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RESULT 44  
 AS1056 15 bp DNA linear PAT 10-MAR-1997  
 LOCUS Sequence 8 from Patent WO9616171.  
 DEFINITION AS1056  
 ACCESSION AS1056  
 VERSION AS1056.1 GI:2303833  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Windass,J.D., Duncan,R.E., Baule,V.J. and Christian,P.D.  
 TITLE TOXINS FROM THE WASP BRACON HEBETOR  
 JOURNAL Patent: WO 9616171-A 8 30-MAY-1996;  
 ZENECA LTD (GB)  
 COMMENT Other publication AU 3877795 960617.  
 FEATURES  
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Query Match 2.0%; Score 12; DB 6; Length 15;  
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QY 246 CTCCTGAGGCC 257  
 Db 3 CTCCTGAGGCC 14

RESULT 45  
 A67408 15 bp DNA linear PAT 05-MAY-1999  
 LOCUS Sequence 33 from Patent WO9744355.  
 DEFINITION A67408  
 ACCESSION A67408  
 VERSION A67408.1 GI:4756348  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Duncan,R.E., Suter,M., Daly,A., Christian,P.D., Windass,J.D. and  
 Claudianos,A.  
 TITLE BIOLOGICAL INSECT CONTROL AGENT  
 JOURNAL Patent: WO 9744355-A 33 27-NOV-1997;  
 ZENECA LTD (GB)  
 FEATURES  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"  
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## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 15;  
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257  
 Db 3 CTCCTGAGGCC 14

RESULT 46  
 A68725 15 bp DNA linear PAT 06-MAY-1999  
 LOCUS Sequence 9 from Patent WO9801757.  
 DEFINITION A68725  
 ACCESSION A68725  
 VERSION A68725.1 GI:4759720  
 KEYWORDS  
 SOURCE unclassified  
 ORGANISM unclassified

REFERENCE unclassified.  
 1 (bases 1 to 15)  
 AUTHORS Ooboun,J.K., Derbyshire,E.J., McCafferty,J.G., Vaughan,T.J. and  
 Johnson,K.S.  
 TITLE LABELLING AND SELECTION OF MOLECULES  
 JOURNAL Patent: WO 9801757-A 9 15-JUN-1998;  
 CAMBRIDGE ANTIBODY TECH (GB)  
 COMMENT Other publication GB 2315125 19980121.  
 FEATURES  
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 /organism="unclassified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 15;  
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257  
 Db 3 CTCCTGAGGCC 14

RESULT 47  
 AR005202 15 bp DNA linear PAT 04-DEC-1998  
 LOCUS Sequence 10 from patent US 5747645.  
 DEFINITION AR005202  
 ACCESSION AR005202  
 VERSION AR005202.1 GI:3966081  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Sprecher,C.A.  
 TITLE Cytoplasmic antiprotease-2 and cytoplasmic antiprotease-3 and  
 coding sequences  
 JOURNAL Patent: US 5747645-A 10 05-MAY-1998;  
 FEATURES  
 source Location/Qualifiers  
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 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257  
 Db 3 CTCCTGAGGCC 14

RESULT 48  
 AR091792 15 bp DNA linear PAT 07-SEP-2000  
 LOCUS Sequence 35 from patent US 5994519.  
 DEFINITION AR091792  
 ACCESSION AR091792  
 VERSION AR091792.1 GI:10018546  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Ooboun,J.Katharine., Derbyshire,E.Joy., McCafferty,J.Gerald.,  
 Vaughan,T.John. and Johnson,K.Stuart.  
 TITLE Labelling and selection of molecules  
 JOURNAL Patent: US 5994519-A 35 30-NOV-1999;  
 FEATURES  
 source Location/Qualifiers  
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 /organism="unknown"  
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## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 15;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14

RESULT 49  
AR126265  
LOCUS AR126265 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 35 from patent US 6180336.  
ACCESSION AR126265  
VERSION AR126265.1 GI:14112858  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Osbourn, J. Katharine., Derbyshire, F. Joy., McCafferty, J. Gerald.,

TITLE Vaughan, T. John, and Johnson, K. Stuart.  
JOURNAL Labelling and selection of molecules  
Patent: US 6180336-A 35 30-JAN-2001;  
FEATURES Location/Qualifiers  
1. 15  
source

ORIGIN /organism="unknown"  
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Query Match 2.0%; Score 12; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14

RESULT 50  
LOCUS 128574 15 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 27 from patent US 5571937.  
ACCESSION 128574  
VERSION 128574.1 GI:1819350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Watanabe, K. A., Ren, W.-Y. and Weil, R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5571937-A 27 05-NOV-1996;  
FEATURES Location/Qualifiers  
1. 15  
source

ORIGIN /organism="unknown"  
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Query Match 2.0%; Score 12; DB 6; Length 15;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTCCTC 186  
Db 13 TTGCTCTCTCCTC 2

RESULT 51  
LOCUS 158736 15 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 27 from patent US 5652350.

ACCESSION 158736  
LOCUS 158736.1 GI:2477974  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Watanabe, K. A., Ren, W.-Y. and Weil, R.  
TITLE Complementary DNA and toxins  
JOURNAL Patent: US 5652350-A 27 29-JUL-1997;  
FEATURES Location/Qualifiers  
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source

ORIGIN /organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTCCTC 186  
Db 13 TTGCTCTCTCCTC 2

RESULT 52  
LOCUS 181235 15 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 10 from patent US 5710026.  
ACCESSION 181235  
VERSION 181235.1 GI:3209525  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Sprecher, C. A.  
TITLE Cytoplasmic antiprotease-2 and cytoplasmic antiprotease-3 and  
coding sequences  
JOURNAL Patent: US 5710026-A 10 20-JAN-1998;  
FEATURES Location/Qualifiers  
1. 15  
source

ORIGIN /organism="unknown"  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
Db 3 CTCCTGGAGCCC 14

RESULT 53  
LOCUS 182215 15 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 10 from patent US 5712117.  
ACCESSION 182215  
VERSION 182215.1 GI:3210512  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Sprecher, C. A.  
TITLE Cytoplasmic antiprotease-2 and coding sequences  
JOURNAL Patent: US 5712117-A 10 27-JAN-1998;  
FEATURES Location/Qualifiers  
1. 15  
source

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ORIGIN /mol_type="unassigned DNA"
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  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 54
AR184255 15 bp DNA linear PAT 20-APR-2002
LOCUS AR184255
DEFINITION Sequence 35 from patent US 6342588.
ACCESSION AR184255
VERSION AR184255.1 GI:20228224
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Osbourn,J.,Katharine., Derbyshire,E.,Joy., McCafferty,J.,Gerald.,
TITLE Vaughn,T.,John. and Johnson,K.,Stuart.
JOURNAL Labelling and selection of molecules
FEATURES
  Patent: US 6342588-A 35 29-JAN-2002;
  Location/Qualifiers
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ORIGIN
Query Match
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  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 55
AR258241 15 bp DNA linear PAT 20-DEC-2002
LOCUS AR258241
DEFINITION Sequence 35 from patent US 6489123.
ACCESSION AR258241
VERSION AR258241.1 GI:27308418
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Osbourn,J.K., Derbyshire,E.J., McCafferty,J.G., Vaughan,T.J. and
TITLE Johnson,K.S.
JOURNAL Labelling and selection of molecules
FEATURES
  Patent: US 6489123-A 35 03-DEC-2002;
  Location/Qualifiers
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      /mol_type="genomic DNA"

ORIGIN
Query Match
  Best Local Similarity 100.0%; Score 12; DB 6; Length 15;
  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 56
AR258241 15 bp DNA linear PAT 20-DEC-2002
LOCUS AR258241
DEFINITION Sequence 35 from patent US 6489123.
ACCESSION AR258241
VERSION AR258241.1 GI:27308418
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Osbourn,J.K., Derbyshire,E.J., McCafferty,J.G., Vaughan,T.J. and
TITLE Johnson,K.S.
JOURNAL Labelling and selection of molecules
FEATURES
  Patent: US 6489123-A 35 03-DEC-2002;
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QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 57
E07495/c 16 bp DNA linear PAT 29-SEP-1997
LOCUS E07495/c
DEFINITION Synthetic DNA for probe.
ACCESSION E07495
VERSION E07495.1 GI:2175633
KEYWORDS JP 1994133799-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Yamamishi,K., Yamamoto,T. and Mori,H.
TITLE ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE B (3754/24) HHV-6) DNA AND
JOURNAL DISCRIMINATION OF SUB-TYPE
  Patent: JP 1994133799-A 4 17-MAY-1994;
  INTERNAL REAGENTS CORP
  OS None
  OC Artificial sequences.
  PN JP 1994133799-A/4
  PD 17-MAY-1994
  PF 27-OCT-1992 JP 1992311416
  PI YAMAMISHI KOICHI, YAMAMOTO TARESHI, MORI HIROYUKI PC
  C12Q1/68,C12Q1/68,C12N15/11,C12N15/38;
  CC strandedness: Single;
  CC topology: linear;
  CC hypothetical: No;
  CC anti-sense: No;
  CC Key
  FT source
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      Location/Qualifiers

BD096388 15 bp DNA linear PAT 27-AUG-2002
LOCUS BD096388
DEFINITION Novel scavenger receptor.
ACCESSION BD096388
VERSION BD096388.1 GI:22641976
KEYWORDS WO 0159107-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 15)
AUTHORS artificial sequences.
JOURNAL Wakiyama,N.
  Novel scavenger receptor
  Patent: WO 0159107-A 18 16-AUG-2001;
  FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA
  OS Artificial Sequence
  PN WO 0159107-A/18
  PD 16-AUG-2001
  PF 08-FEB-2001 WO 2001JP000874
  PR 14-FEB-2000 JP 00P 35155,10-OCT-2000 JP 00P 309068 PI
  NOBUTAKA WAKAMIYA
  PC C12N15/12,C07K14/47,C12N1/21,C12N5/10,C12P21/02,C07K16/28, PC
  C12P21/08,
  PC A01K67/027,A61K45/00,A61P9/10,A61P3/06,A61P3/10 CC Sequence
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  Location/Qualifiers
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        Location/Qualifiers
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Query Match
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QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 58
E07495/c 16 bp DNA linear PAT 29-SEP-1997
LOCUS E07495/c
DEFINITION Synthetic DNA for probe.
ACCESSION E07495
VERSION E07495.1 GI:2175633
KEYWORDS JP 1994133799-A/4.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Yamamishi,K., Yamamoto,T. and Mori,H.
TITLE ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE B (3754/24) HHV-6) DNA AND
JOURNAL DISCRIMINATION OF SUB-TYPE
  Patent: JP 1994133799-A 4 17-MAY-1994;
  INTERNAL REAGENTS CORP
  OS None
  OC Artificial sequences.
  PN JP 1994133799-A/4
  PD 17-MAY-1994
  PF 27-OCT-1992 JP 1992311416
  PI YAMAMISHI KOICHI, YAMAMOTO TARESHI, MORI HIROYUKI PC
  C12Q1/68,C12Q1/68,C12N15/11,C12N15/38;
  CC strandedness: Single;
  CC topology: linear;
  CC hypothetical: No;
  CC anti-sense: No;
  CC Key
  FT source
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      Location/Qualifiers
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FEATURES FT /organism='Artificial sequences',  
source Location/Qualifiers

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/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 496 CATGAATAATCA 507  
Db 12 CATGAATAATCA 1

RESULT 58

LOCUS AR361170 16 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 41 from patent US 6599700.  
ACCESSION AR361170  
VERSION AR361170.1 GI:33768875  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Bellacosa, A.  
TITLE Methods for detection of transition single-nucleotide polymorphisms  
JOURNAL Patent: US 6599700-A 41 29-JUL-2003;  
FEATURES Location/Qualifiers  
source 1.16  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 CTACATCCTTTT 127  
Db 15 CTACATCCTTTT 4

RESULT 59

LOCUS AR040435 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1283 from patent US 5807743.  
ACCESSION AR040435  
VERSION AR040435.1 GI:5959798  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Stinchcomb, D.T. and McGSwigen, J.A.  
TITLE Interleukin-2 receptor gamma-chain ribozymes  
JOURNAL Patent: US 5807743-A 1283 15-SEP-1998;  
FEATURES Location/Qualifiers  
source 1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 CCTGAGGCCCTT 259  
Db 13 CCTGAGGCCCTT 2

RESULT 60

LOCUS BD241420 17 bp DNA linear PAT 17-JUL-2003  
DEFINITION Methods and products related to genotyping and DNA analysis.  
ACCESSION BD241420  
VERSION BD241420.1 GI:33051190  
KEYWORDS JP 2002525127-A/367.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.  
TITLE Methods and products related to genotyping and DNA analysis  
JOURNAL Patent: JP 2002525127-A 367 13-AUG-2002;  
MASSACHUSETTS INSTITUTE OF TECHNOLOGY

COMMENT

OS Homo sapiens (human)  
PN JP 2002525127-A/367  
PD 13-AUG-2002  
PF 24-SEP-1999 JP 2000572407  
PR 25-SEP-1998 US 60/101757  
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC  
C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC  
G01N37/00,  
PC C12N15/00  
CC Methods and products related to genotyping and DNA analysis FH  
Key Location/Qualifiers  
FT source 1.17  
/organism="Homo sapiens (human)".  
FT Location/Qualifiers

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 409 GCCATCATGACC 420  
Db 5 GCCATCATGACC 16

RESULT 61

LOCUS 126836 17 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 59 from patent US 5561041.  
ACCESSION 126836  
VERSION 126836.1 GI:1606706  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Sidransky, D.  
TITLE Nucleic acid mutation detection by analysis of sputum  
JOURNAL Patent: US 5561041-A 59 01-OCT-1996;  
FEATURES Location/Qualifiers  
source 1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 490 GGGCTGCATGAA 501  
Db 13 GGGCTGCATGAA 501

Db 5 GGGCTGCATGAA 16

RESULT 62

LOCUS 127966 17 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 138 from patent US 5567809.

ACCESSION 127966

VERSION 127966.1 GI:1818742

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.

TITLE Methods and reagents for HLA DRbeta DNA typing

JOURNAL Patent: US 5567809-A 138 22-OCT-1996;

FEATURES

source

1. .17

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGAGC 255

Db 1 ACCTCCTGAGC 12

RESULT 63

LOCUS 127987 17 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 159 from patent US 5567809.

ACCESSION 127987

VERSION 127987.1 GI:1818763

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.

TITLE Methods and reagents for HLA DRbeta DNA typing

JOURNAL Patent: US 5567809-A 159 22-OCT-1996;

FEATURES

source

1. .17

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGAGC 255

Db 1 ACCTCCTGAGC 12

RESULT 64

LOCUS 191577 17 bp DNA linear PAT 01-DEC-1998

DEFINITION Sequence 59 from patent US 5726019.

ACCESSION 191577

VERSION 191577.1 GI:3936047

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Sidransky,D.

TITLE Analysis of sputum by amplification and detection of mutant nucleic acid sequences

JOURNAL Patent: US 5726019-A 59 10-MAR-1998;

FEATURES

source

1. .17

/organism="unknown"

/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCATGAA 501

Db 5 GGGCTGCATGAA 16

RESULT 65

LOCUS AX214609/c 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 51 from Patent WO0159103.

ACCESSION AX214609

VERSION AX214609.1 GI:15524652

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 51 16-AUG-2001;

FEATURES

source

1. .17

/organism="synthetic construct"

/mol\_type="unassigned RNA"

/db\_xref="taxon:32630"

/note="Nucleic Acid"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373

Db 17 CTGAGCCCGAGG 6

RESULT 66

LOCUS AX215505/c 17 bp RNA linear PAT 07-SEP-2001

DEFINITION Sequence 947 from Patent WO0159103.

ACCESSION AX215505

VERSION AX215505.1 GI:15525548

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.

TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 947 16-AUG-2001;

FEATURES

source

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/organism="synthetic construct"

/mol\_type="unassigned RNA"

ORIGIN /db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373  
DB 12 CTGAGCCCGAGG 1

RESULT 67  
LOCUS AX216404 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 1846 from Patent WO0159103.  
ACCESSION AX216404  
VERSION AX216404.1 GI:15526465  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
PATENT: WO 0159103-A 1846 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwigen, James (US); Chowrira, Bharat M. (US)

## JOURNAL

FEATURES  
source 1.17  
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/db\_xref="taxon:32630"  
/note="Nucleic Acid"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373  
DB 14 CTGAGCCCGAGG 3

RESULT 68  
LOCUS AX216978 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2420 from Patent WO0159103.  
ACCESSION AX216978  
VERSION AX216978.1 GI:15527039  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
PATENT: WO 0159103-A 2420 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwigen, James (US); Chowrira, Bharat M. (US)

## JOURNAL

FEATURES  
source 1.17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373  
DB 16 CTGAGCCCGAGG 5

RESULT 69  
LOCUS AX216979 17 bp RNA linear PAT 07-SEP-2001  
DEFINITION Sequence 2421 from Patent WO0159103.  
ACCESSION AX216979  
VERSION AX216979.1 GI:15527040  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Blatt, L., McSwigen, J. and Chowrira, B.M.  
TITLE Method and reagent for the modulation and diagnosis of cd20 and  
nogo gene expression  
PATENT: WO 0159103-A 2421 16-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);  
McSwigen, James (US); Chowrira, Bharat M. (US)

## JOURNAL

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source 1.17  
/organism="synthetic construct"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32630"  
/note="Nucleic Acid"

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373  
DB 15 CTGAGCCCGAGG 4

RESULT 70  
LOCUS AX262772 17 bp DNA linear PAT 26-OCT-2001  
DEFINITION Sequence 163 from Patent WO0173002.  
ACCESSION AX262772  
VERSION AX262772.1 GI:16511571  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Kniec, E.B., Gamber, H.B. and Rice, M.C.  
TITLE Targeted chromosomal genomic alterations with modified single  
stranded oligonucleotides  
PATENT: WO 0173002-A 163 04-OCT-2001;  
UNIVERSITY OF DELAWARE (US)

## JOURNAL

FEATURES  
source 1.17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGAGG 27  
DB 3 ATGACCGAGG 14

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RESULT 71
AX262773/c
LOCUS AX262773
DEFINITION Sequence 164 from Patent WO0173002.
ACCESSION AX262773
VERSION AX262773.1 GI:16511572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Kmiec,E.B., Gampel,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 164 04-OCT-2001;
JOURNAL UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
DB 15 ATGAACCGAGG 4

RESULT 72
AX262800
LOCUS AX262800
DEFINITION Sequence 191 from Patent WO0173002.
ACCESSION AX262800
VERSION AX262800.1 GI:16511599
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Kmiec,E.B., Gampel,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 191 04-OCT-2001;
JOURNAL UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
DB 2 ATGAACCGAGG 13

RESULT 73
AX262801/c
LOCUS AX262801/c
DEFINITION Sequence 192 from Patent WO0173002.
ACCESSION AX262801

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VERSION AX262801.1 GI:16511600
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Kmiec,E.B., Gampel,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 192 04-OCT-2001;
JOURNAL UNIVERSITY OF DELAWARE (US)
FEATURES
source
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
DB 16 ATGAACCGAGG 5

RESULT 74
AX460261/c
LOCUS AX460261
DEFINITION Sequence 114 from Patent WO0244736.
ACCESSION AX460261
VERSION AX460261.1 GI:21725885
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Tazi-Ahmini,R., Bavik,C., Ward,S., Duff,G. and Cork,M.
Diagnosis and treatment of disease
Patent: WO 0244736-A 114 06-JUN-2002;
JOURNAL Molecular Skincare Limited (GB)
FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Primer"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 CATCTCGAGCTG 203
DB 17 CATCTCGAGCTG 6

RESULT 75
AX499487/c
LOCUS AX499487
DEFINITION Sequence 794 from Patent EP1259046.
ACCESSION AX499487
VERSION AX499487.1 GI:23381780
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Zhan,J.

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TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 794 07-AUG-2002;

FEATURES  
source  
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Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 386 TGCACCGCGCGC 397  
DB 17 TGCACCGCGCGC 6

RESULT 76  
AX499493/c 17 bp DNA linear PAT 27-SEP-2002

LOCUS AX499493  
DEFINITION Sequence 800 from Patent EP1229046.  
ACCESSION AX499493  
VERSION AX499493.1 GI:23381786  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Zhan, J.  
TITLE Human testis expressed patched like protein  
JOURNAL Patent: EP 1229046-A 800 07-AUG-2002;

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCC 396  
DB 12 CTGCACCGCGCC 1

RESULT 77  
AX4545291 17 bp DNA linear PAT 26-NOV-2002

LOCUS AX4545291  
DEFINITION Sequence 804 from Patent EP1243660.  
ACCESSION AX4545291  
VERSION AX4545291.1 GI:25810502  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.  
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10  
JOURNAL Patent: EP 1243660-A 804 25-SEP-2002;

FEATURES  
source  
1. .17  
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/db\_xref="taxon:9606"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176  
DB 6 CCACGTGAATT 17

RESULT 78  
AX545292 17 bp DNA linear PAT 26-NOV-2002

LOCUS AX545292  
DEFINITION Sequence 805 from Patent EP1243660.  
ACCESSION AX545292  
VERSION AX545292.1 GI:25810503  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.  
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10  
JOURNAL Patent: EP 1243660-A 805 25-SEP-2002;

FEATURES  
source  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176  
DB 5 CCACGTGAATT 16

RESULT 79  
AX545293 17 bp DNA linear PAT 26-NOV-2002

LOCUS AX545293  
DEFINITION Sequence 806 from Patent EP1243660.  
ACCESSION AX545293  
VERSION AX545293.1 GI:25810504  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.  
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10  
JOURNAL Patent: EP 1243660-A 806 25-SEP-2002;

FEATURES  
source  
1. .17  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176  
DB 4 CCACGTGAATT 15

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RESULT 80
LOCUS AX545294 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 807 from Patent EP1243660.
ACCESSION AX545294
VERSION AX545294.1 GI:25810505
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhang,J., Gu,Y. and Nguyen,C.T.
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 807 25-SEP-2002;
          Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176
Db 3 CCACGTGAATT 14

RESULT 81
LOCUS AX545295 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 808 from Patent EP1243660.
ACCESSION AX545295
VERSION AX545295.1 GI:25810506
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Zhang,J., Gu,Y. and Nguyen,C.T.
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 808 25-SEP-2002;
          Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176
Db 2 CCACGTGAATT 13

RESULT 82
LOCUS AX545296 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 809 from Patent EP1243660.
ACCESSION AX545296
VERSION AX545296.1 GI:25810507
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang,J., Gu,Y. and Nguyen,C.T.
TITLE Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 809 25-SEP-2002;
          Aeomica, Inc. (US)
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176
Db 1 CCACGTGAATT 12

RESULT 83
LOCUS AX673640 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2085 from Patent WO03004526.
ACCESSION AX673640
VERSION AX673640.1 GI:29331988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
          reversion, apoptosis and/or resistance to viruses and their use as
          medicines
JOURNAL Patent: WO 03004526-A 2085 16-JAN-2003;
          Molecular Engines Laboratories (FR)
FEATURES
source location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGAG 366
Db 4 CGCAGGCTGAG 15

RESULT 84
LOCUS AX687580 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 312 from Patent EP1281758.
ACCESSION AX687580
VERSION AX687580.1 GI:29410276
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
          mdz12

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JOURNAL Patent: EP 1281758-A 312 05-FEB-2003;
FEATURES
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"
ORIGIN
Query Match
  2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
Db 17 TCCTGGAGCCCC 6

RESULT 85
LOCUS AX687586 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 318 from Patent EP1281758.
ACCESSION AX687586
VERSION AX687586.1 GI:29410282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 318 05-FEB-2003;
Aeomica, Inc. (US)
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGCCCC 257
Db 12 CTCCTGAGCCCC 1

RESULT 86
LOCUS AX688061 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 793 from Patent EP1281758.
ACCESSION AX688061
VERSION AX688061.1 GI:29410759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 793 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445
Db 5 TTTACTGCTGGA 16

RESULT 87
LOCUS AX688062 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 794 from Patent EP1281758.
ACCESSION AX688062
VERSION AX688062.1 GI:29410760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 794 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
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    /db_xref="taxon:9606"
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Query Match
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445
Db 5 TTTACTGCTGGA 16

RESULT 88
LOCUS AX688063 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 795 from Patent EP1281758.
ACCESSION AX688063
VERSION AX688063.1 GI:29410761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
JOURNAL Patent: EP 1281758-A 795 05-FEB-2003;
Aeomica, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445
Db 5 TTTACTGCTGGA 16
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Db 4 TTTACTGCTGGA 15

RESULT 89  
LOCUS AX688064 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 796 from Patent EPI281758.  
ACCESSION AX688064  
VERSION AX688064.1 GI:29410762  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
TITLE mdz12  
JOURNAL Patent: EP 1281758-A 796 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES location/Qualifiers  
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ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445  
Db 3 TTTACTGCTGGA 14

RESULT 90  
LOCUS AX688065 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 797 from Patent EPI281758.  
ACCESSION AX688065  
VERSION AX688065.1 GI:29410763  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
TITLE mdz12  
JOURNAL Patent: EP 1281758-A 797 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445  
Db 2 TTTACTGCTGGA 13

RESULT 91  
LOCUS AX688066 17 bp DNA linear PAT 31-MAR-2003

DEFINITION Sequence 798 from Patent EPI281758.  
ACCESSION AX688066  
VERSION AX688066.1 GI:29410764  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
TITLE mdz12  
JOURNAL Patent: EP 1281758-A 798 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES location/Qualifiers  
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/db\_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445  
Db 1 TTTACTGCTGGA 12

RESULT 92  
LOCUS AX691696 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 4428 from Patent EPI281758.  
ACCESSION AX691696  
VERSION AX691696.1 GI:29414634  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
TITLE mdz12  
JOURNAL Patent: EP 1281758-A 4428 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES location/Qualifiers  
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ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGCGC 376  
Db 17 AGCCCGAGGCGC 6

RESULT 93  
LOCUS AX691697 17 bp DNA linear PAT 31-MAR-2003  
DEFINITION Sequence 4429 from Patent EPI281758.  
ACCESSION AX691697  
VERSION AX691697.1 GI:29414635  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and  
TITLE mdz12  
JOURNAL Patent: EP 1281758-A 4429 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES location/Qualifiers  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 4429 05-FEB-2003;  
Aeomica, Inc. (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGCCCGAGGGGC 376  
Db 16 AGCCCGAGGGGC 5  
RESULT 94  
AX691698 17 bp DNA linear PAT 31-MAR-2003  
LOCUS AX691698  
DEFINITION Sequence 4430 from Patent EP1281758.  
ACCESSION AX691698  
VERSION AX691698.1 GI:29414636  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 4430 05-FEB-2003;  
JOURNAL Aeomica, Inc. (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGCCCGAGGGGC 376  
Db 15 AGCCCGAGGGGC 4  
RESULT 95  
AX691699 17 bp DNA linear PAT 31-MAR-2003  
LOCUS AX691699  
DEFINITION Sequence 4431 from Patent EP1281758.  
ACCESSION AX691699  
VERSION AX691699.1 GI:29414637  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 4431 05-FEB-2003;  
JOURNAL Aeomica, Inc. (US)

FEATURES  
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1.17  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGCCCGAGGGGC 376  
Db 14 AGCCCGAGGGGC 3  
RESULT 96  
AX691700 17 bp DNA linear PAT 31-MAR-2003  
LOCUS AX691700  
DEFINITION Sequence 4432 from Patent EP1281758.  
ACCESSION AX691700  
VERSION AX691700.1 GI:29414638  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 4432 05-FEB-2003;  
JOURNAL Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGCCCGAGGGGC 376  
Db 13 AGCCCGAGGGGC 2  
RESULT 97  
AX691701 17 bp DNA linear PAT 31-MAR-2003  
LOCUS AX691701  
DEFINITION Sequence 4433 from Patent EP1281758.  
ACCESSION AX691701  
VERSION AX691701.1 GI:29414639  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.  
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
TITLE Patent: EP 1281758-A 4433 05-FEB-2003;  
JOURNAL Aeomica, Inc. (US)  
FEATURES  
source Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376  
12 AGCCCGAGGGGC 1

RESULT 98  
AX724214 17 bp DNA linear PAT 08-MAY-2003  
LOCUS Sequence 1901 from Patent WO03025176.  
DEFINITION AX724214  
ACCESSION AX724214.1 GI:30503557  
VERSION  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS 1  
TITLE Teleman, A., Amson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
Patent: WO 03025176-A 1901 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
Location/Qualifiers

FEATURES  
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## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TGAACCTACCT 86  
5 TGAACCTACCT 16

RESULT 99  
AX724376/c 17 bp DNA linear PAT 08-MAY-2003  
LOCUS AX724376  
DEFINITION Sequence 2063 from Patent WO03025176.  
ACCESSION AX724376  
VERSION AX724376.1 GI:30503719  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS 1  
TITLE Teleman, A., Amson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
Patent: WO 03025176-A 2063 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
Location/Qualifiers

FEATURES  
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/organism="Mus musculus"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:10090"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 GAAACCATGAA 468

Db 17 GAAACCATGAA 6

RESULT 100  
AX724877 17 bp DNA linear PAT 08-MAY-2003  
LOCUS AX724877  
DEFINITION Sequence 2564 from Patent WO03025176.  
ACCESSION AX724877  
VERSION AX724877.1 GI:30504220  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE  
AUTHORS 1  
TITLE Teleman, A., Amson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
Patent: WO 03025176-A 2564 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
Location/Qualifiers

FEATURES  
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/organism="Mus musculus"  
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## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGACCTTGCT 141  
6 CTGACCTTGCT 17

RESULT 101  
AX728700 17 bp DNA linear PAT 08-MAY-2003  
LOCUS AX728700  
DEFINITION Sequence 334 from Patent WO03025175.  
ACCESSION AX728700  
VERSION AX728700.1 GI:30508043  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS 1  
TITLE Teleman, A., Amson, R. and Tuijinder, M.  
Sequences involved in phenomena of tumour suppression, tumour  
reversion, apoptosis and/or virus resistance and their use as  
medicines  
Patent: WO 03025175-A 334 27-MAR-2003;  
Molecular Engines Laboratories (FR)  
Location/Qualifiers

FEATURES  
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## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ACCATGAAGA 472  
5 ACCATGAAGA 16

RESULT 102

LOCUS	AX730426	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 2060 from Patent WO03025175.				
ACCESSION	AX730426				
VERSION	AX730426.1 GI:30509769				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1. Telesman, A., Amson, R., and Tuijinder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 2060 27-MAR-2003;				
JOURNAL	Molecular Engines Laboratories (FR)				
FEATURES					
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ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	313 AGCTGAGGATC 324       12 AGCTGAGGATC 1				
RESULT 103					
LOCUS	AX731908	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 3542 from Patent WO03025175.				
ACCESSION	AX731908				
VERSION	AX731908.1 GI:30511251				
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1. Telesman, A., Amson, R., and Tuijinder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines Patent: WO 03025175-A 3542 27-MAR-2003;				
JOURNAL	Molecular Engines Laboratories (FR)				
FEATURES					
source	1..17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"				
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	355 CGAAGGCTGAG 366       4 CGAAGGCTGAG 15				
RESULT 104					
LOCUS	AX734602	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 192 from Patent WO03025177.				
ACCESSION	AX734602				
VERSION	AX734602.1 GI:30513879				

KEYWORDS	Homo sapiens (human)
SOURCE	
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL	Patent: WO 03025177-A 192 27-MAR-2003;
FEATURES	Molecular Engines Laboratories (FR)
source	Location/Qualifiers
1. 17	
/organism="Homo sapiens"	
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/db_xref="taxon:9606"	
ORIGIN	
Query Match	2.0%; Score 12; DB 6; Length 17;
Best Local Similarity	100.0%; Pred. No. 9.1e+05;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	245
Db	5
CCTCCTGGAGCC	16
RESULT 105	
LOCUS	AX734928
DEFINITION	Sequence 518 from Patent WO03025177.
ACCESSION	AX734928
VERSION	AX734928.1 GI:30514205
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1
JOURNAL	Teleman, A., Amson, R. and Tuijinder, M.
FEATURES	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
source	Patent: WO 03025177-A 518 27-MAR-2003;
Location/Qualifiers	
1. 17	
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/mol_type="unassigned DNA"	
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ORIGIN	
Query Match	2.0%; Score 12; DB 6; Length 17;
Best Local Similarity	100.0%; Pred. No. 9.1e+05;
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	418
Db	13
ACCTTCAAAGT	2
RESULT 106	
LOCUS	AX736368/c
DEFINITION	Sequence 1958 from Patent WO03025177.
ACCESSION	AX736368
VERSION	AX736368.1 GI:30515645
KEYWORDS	
SOURCE	
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1
JOURNAL Patent: WO 03025177-A 1958 27-MAR-2003;
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
FEATURES Sequences involved in phenomena of tumour suppression, tumour
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 CCGCAAGGCTGA 365
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14 CCGCAAGGCTGA 3

RESULT 107
LOCUS AX739569 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5159 from Patent WO03025177.
ACCESSION AX739569
VERSION AX739569.1 GI:30518866
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
REFERENCE 1
TITLES Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5159 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCGCAGGCTGAG 366
|||||
4 CCGCAGGCTGAG 15

RESULT 108
LOCUS AX757736 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 1057 from Patent WO03040369.
ACCESSION AX757736
VERSION AX757736.1 GI:32252352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
REFERENCE 1
TITLES Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines

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JOURNAL Patent: WO 03040369-A 1057 15-MAY-2003;
AUTHORS Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 500 AAAATTCACTTC 511
|||||
17 AAAATTCACTTC 6

RESULT 109
LOCUS AX760197 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 3518 from Patent WO03040369.
ACCESSION AX760197
VERSION AX760197.1 GI:32254813
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
REFERENCE 1
TITLES Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 3518 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCGCAGGCTGAG 366
|||||
4 CCGCAGGCTGAG 15

RESULT 110
LOCUS AX762288 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5609 from Patent WO03040369.
ACCESSION AX762288
VERSION AX762288.1 GI:32256904
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
AUTHORS Telerman,A., Amson,R. and Tuijinder,M.
REFERENCE 1
TITLES Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 5609 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1.17
/organism="Homo sapiens"

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ORIGIN
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CCGAGAGCTGAG 366
DB 4 CCGAGAGCTGAG 15

RESULT 111
BD198764 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD198764/c
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION molecule participating in vasculogenic response.
VERSION BD198764.1 GI:33008534
KEYWORDS JP 2002509721-A/1790.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
PATENT: JP 2002509721-A 1790 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/1790
PD 02-APR-2002 JP 2000541291
PR 24-MAR-1999 JP 2000541291
PT 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTGGAGCCCTG 260
DB 12 CTGGAGCCCTG 1

RESULT 112
BD200907 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD200907
DEFINITION Method and reagent for treating diseases or conditions concerning
ACCESSION molecule participating in vasculogenic response.
VERSION BD200907.1 GI:33010677
KEYWORDS JP 2002509721-A/3933.

```

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
PATENT: JP 2002509721-A 3933 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/3933
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PT 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 TTTACCAATTCA 46
DB 6 TTTACCAATTCA 17

RESULT 113
A24633 18 bp DNA linear PAT 02-OCT-1995
LOCUS A24633
DEFINITION SYNTHETIC ECORI primer.
ACCESSION A24633
VERSION A24633.1 GI:1248003
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zabeau,M. and Vos,P.
TITLE Selective restriction fragment amplification : a general method for
JOURNAL DNA fingerprinting
PATENT: EP 0534858-A 43 31-MAR-1993;
KEYGENE N.V.
FEATURES
Location/Qualifiers
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TTACCAATTCA 47

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Db 6 TTACCAATTCOA 17

RESULT 114  
AR076773

LOCUS AR076773 18 bp DNA linear PAT 30-AUG-2000

DEFINITION Sequence 17 from patent US 5959097.

ACCESSION AR076773

VERSION AR076773.1 GI:10003519

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
Monta, B.P. and Cowsett, L.M.  
Antisense modulation of MEK2 expression  
Patent: US 5959097-A 17 28-SEP-1999;

FEATURES  
Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGACTTTGGT 141  
|||||  
6 CTGACTTTGGT 17

Db

RESULT 115  
AR085592

LOCUS AR085592 18 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 28 from patent US 5981732.

ACCESSION AR085592

VERSION AR085592.1 GI:10012359

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
Cowsett, L.M.  
Antisense modulation of G-alpha-13 expression  
Patent: US 5981732-A 28 09-NOV-1999;

FEATURES  
Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGAATCTTCAC 330  
|||||  
7 AGAATCTTCAC 18

Db

RESULT 116  
AR092798

LOCUS AR092798 18 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 13 from patent US 5998206.

ACCESSION AR092798

VERSION AR092798.1 GI:10019550

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
Cowsett, L.M.

TITLE Antisense inhibition of human G-alpha-12 expression

JOURNAL Patent: US 5998206-A 13 07-DEC-1999;

FEATURES  
Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGAATCTTCAC 330  
|||||  
3 AGAATCTTCAC 14

Db

RESULT 117  
AR096294

LOCUS AR096294 18 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 15 from patent US 6007231.

ACCESSION AR096294

VERSION AR096294.1 GI:10024973

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
Vajj, J. and Bishop, R.  
Method of computer aided automated diagnostic DNA test design, and  
apparatus therefor  
Patent: US 6007231-A 15 28-DEC-1999;

FEATURES  
Location/Qualifiers  
1..18  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
|||||  
3 TCGTCTCTCCAG 14

Db

RESULT 118  
BD260529

LOCUS BD260529 18 bp DNA linear PAT 17-JUL-2003

DEFINITION Polymorphic loci that differentiate Escherichia coli O157:H7 from  
other strains.

ACCESSION BD260529

VERSION BD260529.1 GI:33070299

KEYWORDS JP 2002531130-A/8.  
synthetic construct  
artificial sequences.

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 18)  
Tarr, P.I.  
Polymorphic loci that differentiate Escherichia coli O157:H7 from  
other strains

AUTHORS

JOURNAL Patent: JP 2002531130-A 8 24-SEP-2002;  
CHILDREN'S HOSPITAL AND REGIONAL MEDICAL CENTER

COMMENT OS Artificial Sequence  
PN JP 2002531130-A/8  
PD 24-SEP-2002  
PP 08-DEC-1999 JP 2000586917  
PR 08-DEC-1999 US 60/111493  
PT PHILIP I TARR  
PC C12N15/09, C12N15/09, C07K16/12, C12N1/15, C12N1/19, C12N1/21 PC  
C12N5/10, C12N9/04,  
PC

C1201/68,G01N33/53,G01N33/566,G01N33/577// PC  
 C12221/08,  
 PC (C12N5/04,C12R1:19),(C12Q1/68,C12R1:19),C12N15/00,C12N5/00, PC  
 C12N15/00  
 CC primer  
 FH Key  
 FT source  
 Location/Qualifiers  
 1.18  
 /organism="Artificial Sequence",  
 /mol\_type="synthetic construct"  
 /db\_xref="taxon:32630"

## FEATURES

source  
 Location/Qualifiers  
 1.18  
 /organism="Artificial Sequence",  
 /mol\_type="synthetic construct"  
 /db\_xref="taxon:32630"

Query Match  
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 CCGCTACATCTC 197  
 |||||  
 4 CCGCTACATCTC 15

## RESULT 119

LOCUS 127949 18 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 12: from patent US 5567809.  
 ACCESSION 127949  
 VERSION 127949.1 GI:1818725

## KEYWORDS

Unknown.

## SOURCE

Unknown.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.  
 TITLE Methods and reagents for HLA DRbeta DNA typing  
 JOURNAL Patent: US 5567809-A 121 22-OCT-1996;  
 FEATUERS Location/Qualifiers  
 1.18  
 source /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match  
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255  
 |||||  
 2 ACCTCCTGGAGC 13

## RESULT 120

LOCUS 127986 18 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 158 from patent US 5567809.  
 ACCESSION 127986  
 VERSION 127986.1 GI:1818762

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.  
 TITLE Methods and reagents for HLA DRbeta DNA typing  
 JOURNAL Patent: US 5567809-A 158 22-OCT-1996;  
 FEATUERS Location/Qualifiers  
 1.18  
 source /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match  
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255  
 |||||  
 17 ACCTCCTGGAGC 6

## RESULT 121

LOCUS AR361496 18 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 17 from patent US 6599728.  
 ACCESSION AR361496  
 VERSION AR361496.1 GI:33769344

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Morin,G.B., Funk,W.D. and Piatyzek,M.A.  
 TITLE Second mammalian tankyrase  
 JOURNAL Patent: US 6599728-A 17 29-JUL-2003;  
 FEATUERS Location/Qualifiers  
 1.18  
 source /organism="unknown"  
 /mol\_type="genomic DNA"

## ORIGIN

Query Match  
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257  
 |||||  
 3 CTCCTGGAGCCC 14

## RESULT 122

LOCUS AX055650 18 bp DNA linear PAT 13-JAN-2001  
 DEFINITION Sequence 8 from Patent WO0073499.  
 ACCESSION AX055650  
 VERSION AX055650.1 GI:12228790

## KEYWORDS

Unknown.

## SOURCE

Unknown.

## ORGANISM

Unknown.

## REFERENCE

1

Smith,T., Maher,M., Martin,C., Janes,G., Roesau,R. and van der

Weide,M.

Nucleic acid probes and methods for detecting clinically important

fungal pathogens

Patent: WO 0073499-A 8 07-DEC-2000;

INNOGENETICS N.V. (BE) ; Enterprise Ireland (trading as Bioresearch

Ireland) (IE)

Location/Qualifiers

1.18

/organism="Kluyveromyces marxianus"

/mol\_type="unassigned DNA"

/db\_xref="taxon:4911"

## ORIGIN

Query Match  
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCCAG 521  
 |||||  
 6 TCGTCTCCAG 17

RESULT 123  
AX391661/c  
LOCUS AX391661 18 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 42 from Patent EP1184468.  
ACCESSION AX391661  
VERSION AX391661.1 GI:19700267  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 Yamamoto, N.C., Okamoto, T.C. and Suzuki, T.C.  
METHOD for sequencing using probe arrays  
Patent: EP 1184468-A 42 06-MAR-2002;  
CANON KABUSHIKI KAISHA (JP)  
Location/Qualifiers  
1. 18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Sample oligonucleotide"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|  
18 ATGACCGGAGG 7

Db 18 ATGACCGGAGG 7

RESULT 124  
AX391684  
LOCUS AX391684 18 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 65 from Patent EP1184468.  
ACCESSION AX391684  
VERSION AX391684.1 GI:19700290  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE  
1 Yamamoto, N.C., Okamoto, T.C. and Suzuki, T.C.  
METHOD for sequencing using probe arrays  
Patent: EP 1184468-A 65 06-MAR-2002;  
CANON KABUSHIKI KAISHA (JP)  
Location/Qualifiers  
1. 18  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="p53 fragment-Sample oligonucleotide"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

RESULT 125  
AX391810/c  
LOCUS AX391810 18 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 42 from Patent EP1184467.  
ACCESSION AX391810  
VERSION AX391810.1 GI:19700394  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct

REFERENCE  
1 artificial sequences.  
AUTHORS Yamamoto, N., Okamoto, T., Tanaka, S. and Suzuki, T.  
TITLE Screening method for gene variation  
JOURNAL Patent: EP 1184467-A 42 06-MAR-2002;  
CANON KABUSHIKI KAISHA (JP)  
Location/Qualifiers  
1. 18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Sample oligonucleotide"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|  
18 ATGACCGGAGG 7

Db 18 ATGACCGGAGG 7

RESULT 126  
AX391833  
LOCUS AX391833 18 bp DNA linear PAT 23-MAR-2002  
DEFINITION Sequence 65 from Patent EP1184467.  
ACCESSION AX391833  
VERSION AX391833.1 GI:19700417  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.

REFERENCE  
1 Yamamoto, N., Okamoto, T., Tanaka, S. and Suzuki, T.  
TITLE Screening method for gene variation  
JOURNAL Patent: EP 1184467-A 65 06-MAR-2002;  
CANON KABUSHIKI KAISHA (JP)  
Location/Qualifiers  
1. 18  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
/note="p53 fragment-Sample oligonucleotide"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

RESULT 127  
AX398505  
LOCUS AX398505 18 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 1 from Patent EP1184475.  
ACCESSION AX398505  
VERSION AX398505.1 GI:21261206  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 Okamoto, T., Yamamoto, N., Watanabe, H. and Suzuki, T.  
METHOD for making probe, support and apparatus used for the method  
Patent: EP 1184475-A 1 20-MAR-2002;  
CANON KABUSHIKI KAISHA (JP)  
Location/Qualifiers  
1. 18  
/organism="synthetic construct"

ORIGIN

/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Base Oligonucleotide for preparation of a probe"

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|||||  
1 ATGACCGGAGG 12

RESULT 128  
AX453818/c 18 bp DNA linear PAT 06-JUL-2002

LOCUS AX453818  
DEFINITION Sequence 42 from Patent EP1213361.  
ACCESSION AX453818  
VERSION AX453818.1 GI:21713487  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Okamoto, T., Yamamoto, N. and Suzuki, T.  
TITLE Terminal labeled probe array and method of making it  
JOURNAL Patent: EP 1213361-A 42 12-JUN-2002;  
CANON KABUSHIKI KAISHA (JP)  
LOCATION/Qualifiers

FEATURES  
source 1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthesized"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|||||  
18 ATGACCGGAGG 7

RESULT 129  
AX453841 18 bp DNA linear PAT 06-JUL-2002

LOCUS AX453841  
DEFINITION Sequence 65 from Patent EP1213361.  
ACCESSION AX453841  
VERSION AX453841.1 GI:21713510  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Okamoto, T., Yamamoto, N. and Suzuki, T.  
TITLE Terminal labeled probe array and method of making it  
JOURNAL Patent: EP 1213361-A 65 12-JUN-2002;  
CANON KABUSHIKI KAISHA (JP)  
LOCATION/Qualifiers

FEATURES  
source 1.18  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthesized"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
|||||  
1 ATGACCGGAGG 12

RESULT 130  
AX587524 18 bp DNA linear PAT 10-JAN-2003

LOCUS AX587524  
DEFINITION Sequence 34 from Patent WO0236751.  
ACCESSION AX587524  
VERSION AX587524.1 GI:27656340  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1  
AUTHORS Wernet, P.  
TITLE Human cord blood derived unrestricted somatic stem cells (usac)  
JOURNAL Patent: WO 0236751-A 34 10-MAY-2002;  
Kourion Therapeutics GmbH (DE)  
LOCATION/Qualifiers

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/db\_xref="taxon:32630"  
/note="3 primer for the beta actin gene"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGATCTTCA 328  
|||||  
6 TGAGATCTTCA 17

RESULT 131  
BD000011 18 bp DNA linear PAT 31-JAN-2002

LOCUS BD000011  
DEFINITION BD000011  
PROBE-coupling substrate, process for producing the same,  
probe-array, method for detecting target substance, method for  
specifying base sequence of single-stranded nucleic acid in  
sample, and method for quantitating the target substance in the  
sample.

ACCESSION BD000011  
VERSION BD000011.1 GI:18623090  
KEYWORDS JP 2000270896-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Okamoto, H., Yamamoto, N. and Suzuki, T.  
TITLE Probe-coupling substrate, process for producing the same,  
probe-array, method for detecting target substance, method for  
specifying base sequence of single-stranded nucleic acid in sample,  
and method for quantitating the target substance in the sample  
Patent: JP 2000270896-A 1 03-OCT-2000;  
CANON INC AUTEN PHARMACEUT CO LTD  
OS Artificial Sequence  
PN JP 2000270896-A/1  
PD 03-OCT-2000  
PF 28-JAN-1999 JP 1999019915

COMMENT  
JOURNAL  
HISASHI OKAMOTO, NOBUKO YAMAMOTO, TOMOHIRO SUZUKI PC  
C12Q1/68, C12M1/00, C12N15/09, G01N33/566, C12N15/00 CC  
Key  
FT source 1.18  
/organism="Artificial Sequence".  
/mol\_type="genomic DNA"

FEATURES  
source 1.18  
/organism="synthetic construct"

ORIGIN

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ORIGIN                                     /db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
|||||
18 ATGAACCGGAGG 12

Db

RESULT 132
BD000053/c
LOCUS
DEFINITION BD000053 18 bp DNA linear PAT 31-JAN-2002
Probe-coupling substrate, process for producing the same,
specifying base sequence of single-stranded nucleic acid in
sample, and method for quantitating the target substance in the
sample.
ACCESSION BD000053.1 GI:18623132
KEYWORDS JP 200270896-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto,H., Yamamoto,N. and Suzuki,T.
TITLE Probe-coupling substrate, process for producing the same,
probe-array, method for detecting target substance, method for
specifying base sequence of single-stranded nucleic acid in
sample, and method for quantitating the target substance in the
sample.
PATENT: JP 200270896-A 43 03-OCT-2000;
JOURNAL CANON INC ANTEN PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 200270896-A/43
PD 03-OCT-2000
PF 28-JAN-1999 JP 1999019915
PR PI HISASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
CI2Q1/68,C12M1/00,C12N15/09,GOIN33/566,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..18
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source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match                               2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
|||||
18 ATGAACCGGAGG 7

Db

RESULT 133
BD010932
LOCUS
DEFINITION BD010932 18 bp DNA linear PAT 31-JAN-2002
Selective restriction fragment amplification: general DNA
fingerprint method Selective restriction fragment amplification:
general DNA fingerprint method.
ACCESSION BD010932.1 GI:18639305
KEYWORDS JP 2001061486-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)

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```

AUTHORS Szabo,M. and Foss,P.
TITLE Selective restriction fragment amplification: general DNA
fingerprint method
JOURNAL Patent: JP 2001061486-A 42 13-MAR-2001;
COMMENT KEYGENE NV
OS Artificial Sequence
PN JP 2001061486-A/42
PD 13-MAR-2001
PF 25-JUL-2000 JP 2000224187
PR 24-SEP-1991 GB 91402542.4
PI MARK SZABO,PIETER FOSS
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT misc feature (1)..(18).
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source Location/Qualifiers
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/db_xref="taxon:32630"

ORIGIN

Query Match                               2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
|||||
18 ATGAACCGGAGG 7

Db

RESULT 134
BD133664/c
LOCUS BD133664 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for screening mutated gene.
ACCESSION BD133664
VERSION BD133664.1 GI:23228609
KEYWORDS JP 2002071687-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Tanaka,S.
TITLE Method for screening mutated gene
JOURNAL Patent: JP 2002071687-A 42 12-MAR-2002;
COMMENT CANON INC
OS Artificial Sequence
PN JP 2002071687-A/42
PD 12-MAR-2002
PF 31-AUG-2000 JP 2000263396
PR PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,SHINYA TANAKA
PC GOIN33/53,C12M1/00,C12N15/09,C12Q1/68,GOIN33/566,PC
G01N37/00,
PC C12N15/00
CC Sample oligonucleotide
FH Key Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
1..18 /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match                               2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
|||||
18 ATGAACCGGAGG 7

Db

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RESULT 135
BD135697/c
LOCUS
DEFINITION BD135697 18 bp DNA linear PAT 18-SEP-2002
ACCESSION BD135697
VERSION BD135697.1 GI:23230642
KEYWORDS JP 2002065274-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.
TITLE Method for detecting subjective component in specimen sample, and
JOURNAL substrate for detecting subjective component in specimen sample, and
PATENT: JP 2002065274-A 1 05-MAR-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002065274-A/1
PD 05-MAR-2002
PI 31-AUG-2000 JP 2000263395
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,AKIRA SHIMIZU
PC C12N15/09,C12M1/00,C12M1/40,C1201/68,G01N31/22,G01N33/53,PC
G01N33/566,
PC G01N35/02,G01N35/10,G01N37/00,C12N15/00,G01N35/06 CC DNA
probe for hybridizing with gene encoding p53 FH Key
Location/Qualifiers
FT source
FT 1..18
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
|||
|||
|||
Db 18 ATGAACCGGAGG 7

RESULT 136
BD135742/c
LOCUS
DEFINITION BD135742 18 bp DNA linear PAT 18-SEP-2002
ACCESSION BD135742
VERSION BD135742.1 GI:23230687
KEYWORDS JP 2002065274-A/46.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.
TITLE Method for detecting subjective component in specimen sample, and
JOURNAL substrate for detecting subjective component in specimen sample, and
PATENT: JP 2002065274-A 46 05-MAR-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002065274-A/46
PD 05-MAR-2002
PI 31-AUG-2000 JP 2000263395
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,AKIRA SHIMIZU
PC C12N15/09,C12M1/00,C12M1/40,C1201/68,G01N31/22,G01N33/53,PC
G01N33/566,
PC G01N35/02,G01N35/10,G01N37/00,C12N15/00,G01N35/06 CC DNA
probe for hybridizing with gene encoding
mutated p53;named

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FEATURES	source	Location/Qualifiers
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CC		in Table 1
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		/mol_type="genomic DNA"
		/db_xref="taxon:32630"
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Best Local Similarity	100.0%; Pred. No. 9.1e+05;	
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY		
	16 ATGAACCGGAGG 27	
	18 ATGAACCGGAGG 7	
Db		
RESULT 137		
BD1610C8/c	18 bp DNA linear PAT 17-JAN-2003	
LOCUS		
DEFINITION	Terminal-labeled probe-array and method for preparing it, and	
ACCESSION	BD161008	
KEYWORDS	method for evaluating target mass using the same.	
SOURCE	JP 2002153284-A/42.	
ORGANISM	synthetic construct	
	artificial sequence	
	1 (bases 1 to 18)	
AUTHORS	Okamoto,T., Yamamoto,N. and Suzuki,T.	
TITLE	Terminal-labeled probe-array and method for preparing it, and	
JOURNAL	method for evaluating target mass using the same	
	Patent: JP 2002153284-A 42 28-MAY-2002;	
	CANON INC	
COMMENT		
	OS Artificial Sequence	
	PN JP 2002153284-A/42	
	PD 28-MAY-2002	
	PF 24-NOV-2000 JP 2000357446	
	PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC	
	C12N15/09,G12Q1/68,G01N31/22,G01N33/53,G01N33/56,G01N37/00, PC	
	C12N15/00	
	CC Description of Artificial Sequence:Synthesized FH Key	
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FT		Location/Qualifiers
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		/mol_type="genomic DNA"
		/db_xref="taxon:32630"
ORIGIN		
Query Match	2.0%; Score 12; DB 6; Length 18;	
Best Local Similarity	100.0%; Pred. No. 9.1e+05;	
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY		
	16 ATGAACCGGAGG 27	
	18 ATGAACCGGAGG 7	
Db		
RESULT 138		
BD1610J31	18 bp DNA linear PAT 17-JAN-2003	
LOCUS		
DEFINITION	Terminal-labeled probe-array and method for preparing it, and	
ACCESSION	BD1610J31	
KEYWORDS	method for evaluating target mass using the same.	
	JP 2002153284-A/65.	

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Okamoto,T., Yamamoto,N. and Suzuki,T.  
TITLE Terminal-labeled probe-array and method for preparing it, and method for evaluating target mass using the same  
JOURNAL Patent: JP 2002153284-A 65 28-MAY-2002;  
COMMENT CANON INC  
OS Artificial Sequence  
PN JP 2002153284-A/65  
PD 28-MAY-2002  
PI 24-NOV-2000 JP 2000357446  
PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC  
C12N15/09,C12Q1/68,G01N31/22,G01N33/53,G01N33/566,G01N37/00, PC  
C12N15/00  
CC Description of Artificial Sequence:Synthesized FH Key  
FT Location/Qualifiers  
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Location/Qualifiers  
1..18  
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/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGACCGGAGG 27  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

RESULT 139  
BD162058/c  
LOCUS BD162058 18 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method for detecting nucleic acid.  
ACCESSION BD162058  
VERSION BD162058.1 GI:27867816  
KEYWORDS JP 2002176999-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Suzuki,T.  
TITLE Method for detecting nucleic acid  
JOURNAL Patent: JP 2002176999-A 1 25-JUN-2002;  
COMMENT CANON INC  
OS Artificial Sequence  
PN JP 2002176999-A/1  
PD 25-JUN-2002  
PI 12-DEC-2000 JP 2000377349  
PI TOMOHIRO SUZUKI  
PC C12Q1/68,C07H21/04,C12N15/09,G01N33/53,G01N33/566,G01N33/58,  
PC C12N15/00  
CC Target gene fragment for probe hybridization FH Key  
FT Location/Qualifiers  
FT source 1..18  
Location/Qualifiers  
1..18  
/organism='Artificial Sequence'.  
/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGACCGGAGG 27  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

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/mol\_type='genomic DNA'  
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Qy 16 ATGACCGGAGG 27  
16 ATGACCGGAGG 27  
18 ATGACCGGAGG 7

Db 18 ATGACCGGAGG 7

RESULT 140  
BD162059  
LOCUS BD162059 18 bp DNA linear PAT 17-JAN-2003  
DEFINITION Method for detecting nucleic acid.  
ACCESSION BD162059  
VERSION BD162059.1 GI:27867817  
KEYWORDS JP 2002176999-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Suzuki,T.  
TITLE Method for detecting nucleic acid  
JOURNAL Patent: JP 2002176999-A 2 25-JUN-2002;  
COMMENT CANON INC  
OS Artificial Sequence  
PN JP 2002176999-A/2  
PD 25-JUN-2002 JP 2000377349  
PI 12-DEC-2000 JP 2000377349  
PI TOMOHIRO SUZUKI  
PC C12Q1/68,C07H21/04,C12N15/09,G01N33/53,G01N33/566,G01N33/58,  
PC C12N15/00  
CC hybridization probe  
FH Key  
FT Location/Qualifiers  
FT source 1..18  
Location/Qualifiers  
1..18  
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/mol\_type='genomic DNA'  
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ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGACCGGAGG 27  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

RESULT 141  
BD167503/c  
LOCUS BD167503 18 bp DNA linear PAT 17-JAN-2003  
DEFINITION A method of analyzing a base sequence of a nucleic acid.  
ACCESSION BD167503  
VERSION BD167503.1 GI:27873315  
KEYWORDS WO 0233068-A/42.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Yamamoto,N., Okamoto,T. and Suzuki,T.  
TITLE A method of analyzing a base sequence of a nucleic acid  
JOURNAL Patent: WO 0233068-A 42 25-APR-2002;  
COMMENT CANON KK,NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI  
OS Artificial Sequence  
PN WO 0233068-A/42  
PD 25-APR-2002  
PI 18-OCT-2000 WO 2000JP007244  
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI PC  
C12N15/09,C12Q1/68,G01N33/566,G01N33/53  
CC Sample oligonucleotide  
FH Key  
FT Location/Qualifiers  
FT source 1..18  
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/mol\_type='genomic DNA'  
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ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGACCGGAGG 27  
1 ATGACCGGAGG 12

Db 1 ATGACCGGAGG 12

FEATURES  
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Location/Qualifiers  
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/organism='synthetic construct'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32630'

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source
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

RESULT 142
BD174790 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION liquid discharge device for production of probe carrier, device for
production of probe carrier using the liquid discharge device, and
process for producing the probe carrier.
ACCESSION BD174790
VERSION BD174790.1 GI:29120482
KEYWORDS JP 2002257694-A/1.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaneko,M. and Watanabe,H.
TITLE liquid discharge device for production of probe carrier, device for
production of probe carrier using the liquid discharge device, and
process for producing the probe carrier
PATENT: JP 2002257694-A 1 11-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002257694-A/1
PD 11-SEP-2002
PF 28-FEB-2001 JP 2001055970
PI MINO KANEKO,HIDENORI WATANABE
PC G01N35/10,B41J2/05,C12M1/00,C12N15/09,G01N33/53,G01N33/566,PC
G01N35/10
PC G01N37/00,B41J3/04,C12N15/00,G01N35/06
CC Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1.18
Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

RESULT 143
BD174965 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION Process for producing probe carrier using liquid discharge device
and device used for this process.
ACCESSION BD174965
VERSION BD174965.1 GI:29120659
KEYWORDS JP 2002257836-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE
1 (bases 1 to 18)
AUTHORS Okamoto,T.
TITLE Process for producing probe carrier using liquid discharge device
and device used for this process
PATENT: JP 2002257836-A 1 11-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002257836-A/1
PD 11-SEP-2002
PF 28-FEB-2001 JP 2001055971
PI TADASHI OKAMOTO
PC G01N35/10,B41J2/01,B41J2/05,C12M1/00,C12N15/09,G01N37/00,PC
G01N35/06
PC B41J3/04,B41J3/04,C12N15/00
CC Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1.18
Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

RESULT 144
BD175058 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION A method of preparing a probe array.
ACCESSION BD175058
VERSION BD175058.1 GI:29120752
KEYWORDS JP 2002253251-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaneko,M. and Watanabe,H.
TITLE A method of preparing a probe array
PATENT: JP 2002253251-A 1 10-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002253251-A/1
PD 10-SEP-2002
PF 28-FEB-2001 JP 2001055972
PI MINO KANEKO,HIDENORI WATANABE
PC C12N15/09,C12M1/00,G01N33/53,G01N33/566,G01N37/00,C12N15/00,CC
Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1.18
Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
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1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

```

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RESULT 145
BD176986/c 18 bp DNA linear PAT 16-APR-2003
LOCUS BD176986 Method of analyzing nucleic acid base sequence.
DEFINITION BD176986
ACCESSION BD176986
VERSION BD176986.1 GI:30014245
KEYWORDS JP 2002306166-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,H. and Suzuki,T.
TITLES Method of analyzing nucleic acid base sequence
JOURNAL Patent: JP 2002306166-A 42 22-OCT-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002306166-A/42
PD 22-OCT-2002
PE 31-AUG-2000 JP 200263506
PI NOBUKO YAMAMOTO,HISASHI OKAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12O1/68//C12M1/00,C12N15/00
CC Sample originonucleotide
FH Key Location/Qualifiers
FT source 1.18
/organism='Artificial Sequence'.
FEATURES
source 1.18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No.9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 7
Db
RESULT 146
BD177274 18 bp DNA linear PAT 16-APR-2003
LOCUS BD177274 A method of preparing a probe array and a device used therefor.
DEFINITION BD177274
ACCESSION BD177274
VERSION BD177274.1 GI:30014535
KEYWORDS JP 2002318232-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Watanabe,H., Okamoto,T., Yamamoto,N. and Suzuki,T.
TITLES A method of preparing a probe array and a device used therefor
JOURNAL Patent: JP 2002318232-A 1 31-OCT-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002318232-A/1
PD 31-OCT-2002
PE 18-SEP-2001 JP 2001283190
PI HIDENORI WATANABE,TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
G01N33/53,G01N37/00//C12M1/00,C12N15/09,C12N15/00 CC Base
Oligonucleotide for preparation of a probe FH Key
Location/Qualifiers
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source 1.18
Location/Qualifiers
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QY 16 ATGACCGGAGG 27
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1 ATGACCGGAGG 12
Db
RESULT 147
BD187511 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD187511 Probe carrier, Method and Apparatus for producing probe carrier.
DEFINITION BD187511
ACCESSION BD187511
VERSION BD187511.1 GI:32997250
KEYWORDS JP 2003014773-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLES Probe carrier, Method and Apparatus for producing probe carrier
JOURNAL Patent: JP 2003014773-A 1 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/1
PD 15-JAN-2003
PE 28-MAR-2002 JP 200293024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC
Oligonucleotide to be hybridized with the designed CC
oligonucleotide
CC 'gatggcctccggttcac'
FH Key Location/Qualifiers
FT source 1.18
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/mol_type='genomic DNA'
/db_xref='taxon:32630'
FEATURES
source 1.18
Location/Qualifiers
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No.9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12
Db
RESULT 148
BD187512 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD187512 Probe carrier, Method and Apparatus for producing probe carrier.
DEFINITION BD187512
ACCESSION BD187512
VERSION BD187512.1 GI:32997251
KEYWORDS JP 2003014773-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLES Probe carrier, Method and Apparatus for producing probe carrier
JOURNAL Patent: JP 2003014773-A 2 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/2
PD 15-JAN-2003
PE 28-MAR-2002 JP 200293024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC
Oligonucleotide used as a probe

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to be stabilized on a  
CC carrier  
Location/Qualifiers.  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGAGG 27  
18 ATGACCGAGG 7

Db

RESULT 149  
LOCUS A57967 19 bp DNA linear PAT 05-MAR-1998  
DEFINITION Sequence 33 from Patent EP0743364.  
ACCESSION A57967  
VERSION A57967.1 GI:3713737  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
1 Narwa,R. and Roques,P.  
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding fragments and their application as reactives for risk evaluation of HIV-1 mother-foetal transmission  
JOURNAL Patent: EP 0743364-A 33 20-NOV-1996;  
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)  
FEATURES Other publication FR 2734281 961122.  
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/db\_xref="taxon:32644"

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Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTC 186  
4 TTGCTCTCTC 15

Db

RESULT 150  
LOCUS A57968 19 bp DNA linear PAT 05-MAR-1998  
DEFINITION Sequence 34 from Patent EP0743364.  
ACCESSION A57968  
VERSION A57968.1 GI:3713738  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
1 Narwa,R. and Roques,P.  
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding fragments and their application as reactives for risk evaluation of HIV-1 mother-foetal transmission  
JOURNAL Patent: EP 0743364-A 34 20-NOV-1996;  
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)  
FEATURES Other publication FR 2734281 961122.  
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/db\_xref="taxon:32644"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTC 186  
4 TTGCTCTCTC 15

Db

RESULT 151  
LOCUS A57969 19 bp DNA linear PAT 05-MAR-1998  
DEFINITION Sequence 35 from Patent EP0743364.  
ACCESSION A57969  
VERSION A57969.1 GI:3713739  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
1 Narwa,R. and Roques,P.  
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding fragments and their application as reactives for risk evaluation of HIV-1 mother-foetal transmission  
JOURNAL Patent: EP 0743364-A 35 20-NOV-1996;  
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)  
FEATURES Other publication FR 2734281 961122.  
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/db\_xref="taxon:32644"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTC 186  
3 TTGCTCTCTC 14

Db

RESULT 152  
LOCUS A91527 19 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 54 from Patent WO9824928.  
ACCESSION A91527  
VERSION A91527.1 GI:6740482  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
1 (bases 1 to 19)  
Pallisgaard,N. and Hokland,P.  
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES  
JOURNAL Patent: WO 9824928-A 54 11-JUN-1998;  
COMMENT PATLISGAARD NIELS (DK); HOKLAND PETER (DK)  
FEATURES Location/Qualifiers  
source 1.19  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 TTCTGCGAGCGA 301  
 DB 17 TTCTGCGAGCGA 6

RESULT 153  
 LOCUS AR299567/c 19 bp DNA linear PAT 12-JUN-2003  
 DEFINITION Sequence 11302 from patent US 6537751.  
 ACCESSION AR299567  
 VERSION AR299567.1 GI:31686851  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.  
 TITLE Biallelic markers for use in constructing a high density  
 disequilibrium map of the human genome  
 JOURNAL Patent: US 6537751-A 11302 25-MAR-2003;  
 FEATURES Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTCC 187  
 DB 15 TGCTCTTCTCC 4

RESULT 154  
 LOCUS AX023306 19 bp DNA linear PAT 15-SEP-2000  
 DEFINITION Sequence 14 from Patent WO0015788.  
 ACCESSION AX023306  
 VERSION AX023306.1 GI:10183718  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1  
 AUTHORS Moroz,C.  
 TITLE Dna sequence encoding oncofetal ferritin protein  
 JOURNAL Patent: WO 0015788-A 14 23-MAR-2000;  
 MOROZ CHAYA (IL) ; GARDINO INVESTMENT N V (NL)  
 FEATURES Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGCC 257  
 DB 7 CTCCTGAGCC 18

RESULT 155  
 LOCUS AX093498 19 bp DNA linear PAT 30-MAR-2001  
 DEFINITION Sequence 28 from Patent WO0118198.  
 ACCESSION AX093498

VERSION AX093498.1 GI:13509937  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Weissenbach,J. and Hazan,J.  
 TITLE Cloning, expression and characterisation of the spg4 gene  
 responsible for the most frequent form of autosomal spastic  
 paraplegia  
 JOURNAL Patent: WO 0118198-A 28 15-MAR-2001;  
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
 FEATURES Location/Qualifiers  
 source 1..19  
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 /db\_xref="taxon:32630"  
 /note="Amorce"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGAATACCTT 452  
 DB 1 CTGAATACCTT 12

RESULT 156  
 LOCUS AX247496 19 bp DNA linear PAT 28-SEP-2001  
 DEFINITION Sequence 7 from Patent WO0164923.  
 ACCESSION AX247496  
 VERSION AX247496.1 GI:15862165  
 KEYWORDS  
 SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)  
 ORGANISM Agrobacterium tumefaciens  
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
 REFERENCE 1  
 AUTHORS Dumas,F., van Gelder,P., Duckely,M., Hohn,B. and Pelczar,P.  
 TITLE Vire2-mediated trans-membrane delivery systems  
 JOURNAL Patent: WO 0164923-A 7 07-SEP-2001;  
 Novartis Research Foundation (CH) ; Universitaet Basel (CH)  
 FEATURES Location/Qualifiers  
 source 1..19  
 /organism="Agrobacterium tumefaciens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:358"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTGATGACCGG 24  
 DB 3 TTGATGACCGG 14

RESULT 157  
 LOCUS AX287545 19 bp DNA linear PAT 21-NOV-2001  
 DEFINITION Sequence 8 from Patent WO0168853.  
 ACCESSION AX287545  
 VERSION AX287545.1 GI:117049315  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 artificial sequences.  
 REFERENCE 1  
 AUTHORS Roden,R. and Neore,H.

TITLE Immunogenic ovarian cancer genes  
JOURNAL Patent: WO 0168853-A 8 20-SEP-2001;  
The Johns Hopkins University School of Medicine (US)  
FEATURES  
source  
1. .19  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic Primer"  
ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 317 TGAGATCTTCA 328  
Db 8 TGAGATCTTCA 19  
RESULT 158  
AX763549 19 bp DNA linear PAT 25-JUN-2003  
LOCUS AX763549  
DEFINITION Sequence 62 from Patent WO03040366.  
ACCESSION AX763549  
VERSION AX763549.1 GI:32257984  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and  
Dautry, F.  
TITLE Inhibitor oligonucleotides and their use for specific repression of  
a gene  
JOURNAL Patent: WO 03040366-A 62 15-MAY-2003;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
FEATURES  
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1. .19  
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Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGAGG 27  
Db 3 ATGAACCGAGG 14  
RESULT 159  
AX763550 19 bp DNA linear PAT 25-JUN-2003  
LOCUS AX763550  
DEFINITION Sequence 63 from Patent WO03040366.  
ACCESSION AX763550  
VERSION AX763550.1 GI:32257985  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and  
Dautry, F.  
TITLE Inhibitor oligonucleotides and their use for specific repression of  
a gene  
JOURNAL Patent: WO 03040366-A 63 15-MAY-2003;

FEATURES  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
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misc\_feature 1. .19  
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGAGG 27  
Db 3 ATGAACCGAGG 14  
RESULT 160  
AX763551 19 bp DNA linear PAT 25-JUN-2003  
LOCUS AX763551  
DEFINITION Sequence 64 from Patent WO03040366.  
ACCESSION AX763551  
VERSION AX763551.1 GI:32257986  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and  
Dautry, F.  
TITLE Inhibitor oligonucleotides and their use for specific repression of  
a gene  
JOURNAL Patent: WO 03040366-A 64 15-MAY-2003;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
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misc\_feature 1. .19  
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ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 ATGAACCGAGG 27  
Db 3 ATGAACCGAGG 14  
RESULT 161  
AX822525 19 bp DNA linear PAT 11-DEC-2003  
LOCUS AX822525/c  
DEFINITION Sequence 417 from Patent EP1340818.  
ACCESSION AX822525  
VERSION AX822525.1 GI:39749153  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,  
Rufan, T. and Schmitt, A.  
TITLE Method and nucleic acids for the analysis of a colon cell  
proliferative disorder  
JOURNAL Patent: EP 1340818-A 417 03-SEP-2003;  
Epigenomics AG (DE)  
FEATURES  
Location/Qualifiers

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/note="Detection primer for CDH1"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312  
DB 12 AACCCCAACCTC 1

RESULT 162  
AX826165/c  
LOCUS AX826165 19 bp DNA linear PAT 11-DEC-2003  
DEFINITION Sequence 417 from Patent WO03072821.  
ACCESSION AX826165  
VERSION AX826165.1 GI:39751679  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,  
Rujan, T. and Schmitt, A.  
TITLE Method and nucleic acids for the analysis of a colon cell  
JOURNAL proliferative disorder  
Patent: WO 03072821-A 417 04-SBP-2003;  
FEATURES  
source 1.19  
Location/Qualifiers  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312  
DB 12 AACCCCAACCTC 1

RESULT 163  
BD023309/c  
LOCUS BD023309 19 bp DNA linear PAT 27-AUG-2002  
DEFINITION Method for detecting abnormality in chromosome.  
ACCESSION BD023309  
VERSION BD023309.1 GI:22564532  
KEYWORDS JP 2001505428-A/54.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE 1 (bases 1 to 19)  
JOURNAL Parlagard, N. and Hokurano, P.  
Patent: JP 2001505428-A 54 24-APR-2001;  
COMMENT  
PI NEILS PARISGARD  
PD 24-APR-2001  
PF 08-DEC-1997 JP 1998525090  
PC C12N15/09, C12N15/66, G01N33/50, C12N15/00  
CC Strandedness: Single;  
Topology: Linear;

CC /desc = 'DNA (synthetic)'  
FH Key Location/Qualifiers  
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ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 TTCTGCGAGGGA 301  
DB 17 TTCTGCGAGGGA 6

RESULT 164  
A82447/c  
LOCUS A82447 20 bp DNA linear PAT 21-JAN-2000  
DEFINITION Sequence 35 from Patent WO9854360.  
ACCESSION A82447  
VERSION A82447.1 GI:6732195  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Plasow, G.S. and Wales, R.  
TITLE METHODS FOR ANALYZING ANIMAL PRODUCTS  
JOURNAL Patent: WO 9854360-A 35 03-DEC-1998;  
FEATURES  
source 1.20  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGAG 254  
DB 20 CACCTCCTGGAG 9

RESULT 165  
AR085567  
LOCUS AR085567 20 bp DNA linear PAT 01-SBP-2000  
DEFINITION Sequence 3 from patent US 5981732.  
ACCESSION AR085567  
VERSION AR085567.1 GI:10012334  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1  
AUTHORS Cowsett, L.M.  
TITLE Antisense modulation of G-alpha-13 expression  
JOURNAL Patent: US 5981732-A 3 09-NOV-1999;  
FEATURES  
source 1.20  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330  
Db 9 AGGATCTTCACC 20  
RESULT 166  
LOCUS AR097384 20 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 8 from patent US 6071726.  
ACCESSION AR097384  
VERSION AR097384.1 GI:12806114  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.  
TITLE Method, reagents and kit for diagnosis and targeted screening for p53 mutations  
JOURNAL Patent: US 6071726-A 8 06-JUN-2000;  
FEATURES Location/Qualifiers  
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Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TCCTCTCTCCAG 521  
Db 9 TCCTCTCTCCAG 20  
RESULT 167  
LOCUS AR097385/C 20 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6071726.  
ACCESSION AR097385  
VERSION AR097385.1 GI:12806115  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.  
TITLE Method, reagents and kit for diagnosis and targeted screening for p53 mutations  
JOURNAL Patent: US 6071726-A 9 06-JUN-2000;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TCCTCTCTCCAG 521  
Db 18 TCCTCTCTCCAG 7  
RESULT 168  
LOCUS AR099487 20 bp DNA PAT 14-FEB-2001  
DEFINITION Sequence 14 from patent US 6077833.  
ACCESSION AR099487  
VERSION AR099487.1 GI:12809253  
KEYWORDS  
SOURCE Unknown.

ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
JOURNAL Patent: US 6077833-A 14 20-JUN-2000;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 247 TCCTGAGCCCC 258  
Db 6 TCCTGAGCCCC 17  
RESULT 169  
LOCUS AR137400 20 bp DNA PAT 16-JUN-2001  
DEFINITION Sequence 15 from patent US 6197507.  
ACCESSION AR137400  
VERSION AR137400.1 GI:14478909  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Berg,T., Tollerud,O.Kristien. and Nilsen,O.  
TITLE Genetic test for .alpha.-mannosidosis  
JOURNAL Patent: US 6197507-A 15 06-MAR-2001;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 378 GCGCGGCTGCA 389  
Db 7 GCGCGGCTGCA 18  
RESULT 170  
LOCUS AR143130/C 20 bp DNA PAT 08-AUG-2001  
DEFINITION Sequence 21 from patent US 6204055.  
ACCESSION AR143130  
VERSION AR143130.1 GI:15104416  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M. and Marcusson,E.G.  
TITLE Antisense inhibition of Fas mediated signaling  
JOURNAL Patent: US 6204055-A 21 20-MAR-2001;  
FEATURES Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"  
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Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred.No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGATGCTCTT 182  
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20 GGATGCTCTT 9

Db 20 GGATGCTCTT 9

RESULT 171  
AR178768  
LOCUS AR178768 20 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 14 from patent US 6319906.  
ACCESSION AR178768  
VERSION AR178768.1 GI:20219906  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
JOURNAL Patent: US 6319906-A 14-20-NOV-2001;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258  
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6 TCCTGGAGCCCC 17

Db 6 TCCTGGAGCCCC 17

RESULT 172  
AR178952  
LOCUS AR178952 20 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 198 from patent US 6319906.  
ACCESSION AR178952  
VERSION AR178952.1 GI:20220090  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett,C.Frank. and Vickers,T.A.  
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein  
JOURNAL Patent: US 6319906-A 198-20-NOV-2001;  
FEATURES  
source Location/Qualifiers  
1..20  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258  
|||||  
5 TCCTGGAGCCCC 16

Db 5 TCCTGGAGCCCC 16

RESULT 173  
BD230144/c  
LOCUS BD230144 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Total genome radiation hybrid map of canine genome and its use for identification of interesting genes.  
ACCESSION BD230144

VERSION BD230144.1 GI:33039914  
KEYWORDS JP 2002530091-A/13.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE  
AUTHORS Galibert,F. and Andre,C.  
TITLE Total genome radiation hybrid map of canine genome and its use for identification of interesting genes  
JOURNAL Patent: JP 2002530091-A 13 17-SEP-2002;  
COMMENT CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE  
OS Canis familiaris (dog)  
PN JP 2002530091-A/13  
PD 17-SEP-2002  
PF 15-NOV-1998 JP 2000582596  
PI 13-NOV-1998 US 60/108193  
PI FRANCIS GALIBERT,CATHERINE ANDRE  
PC C12N15/09,C12Q1/68,C12N15/00  
CC Rem1023

FEATURES  
source Location/Qualifiers  
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/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9615"

ORIGIN  
Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 GGAAGGGCTGCA 497  
|||||  
17 GGAAGGGCTGCA 6

Db 17 GGAAGGGCTGCA 6

RESULT 174  
BD249305/c  
LOCUS BD249305 20 bp DNA linear PAT 17-JUL-2003  
DEFINITION Antisense modulation of FAS mediated signaling.  
ACCESSION BD249305  
VERSION BD249305.1 GI:33059075  
KEYWORDS JP 2002540812-A/20.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dean,N.M. and Marcussen,E.G.  
TITLE Antisense modulation of FAS mediated signaling  
JOURNAL Patent: JP 2002540812-A 20 03-DEC-2002;  
COMMENT ISIS PHARMACEUTICALS INC  
OS Artificial Sequence  
PN JP 2002540812-A/20  
PD 03-DEC-2002  
PF 10-APR-2000 JP 2000610483  
PR 12-APR-1999 US 09/290640  
PI NICHOLAS M DEAN,ERIC G MARCUSSEN  
PC C12N15/09,A61K31/7088,A61K31/7115,A61K31/712,A61K31/7125, PC  
A61K48/00,  
PC A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06, PC  
C12N15/00,  
CC C12N5/00  
PC Synthetic Sequence  
FH Key Location/Qualifiers  
FT source 1..20  
/organism="Artificial Sequence".  
1..20  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="genomic DNA"

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ORIGIN
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGATTGCTCTT 182
DB 20 GGATTGCTCTT 9

RESULT 175
E06107 20 bp DNA linear PAT 29-SEP-1997
LOCUS Oligonucleotide specific to subtype Pt of Hepatitis C virus.
DEFINITION E06107
ACCESSION E06107
VERSION E06107.1 GI:2174294
KEYWORDS JP 199337000-A/31.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Chayama,K. and Kumada,H.
TITLE METHOD FOR EXAMINING C TYPE HEPATITIS VIRUS AND PRIMER SET USED FOR
THE SAME
JOURNAL Patent: JP 199337000-A 31 21-DEC-1993;
CHAYAMA KAZUAKI
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
OS Hepatitis C virus
PN JP 199337000-A/31
PD 21-DEC-1993
PE 04-JUN-1992 JP 1992168226
FI CHAYAMA KAZUAKI, KOMADA HIROMITSU
PC C12Q1/68, C12N15/10, C12N15/11, C12Q1/70;
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
Location/Qualifiers
source 1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"

ORIGIN
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TTACCAATTCAA 47
DB 8 TTACCAATTCAA 19

RESULT 176
I25689 20 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 8 from patent US 5552283.
DEFINITION I25689
ACCESSION I25689
VERSION I25689.1 GI:1605559
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for
p53 mutations
JOURNAL Patent: US 5552283-A 8 03-SEP-1996;
FEATURES Location/Qualifiers
source 1..20

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ORIGIN
/mol_type="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
DB 9 TCGTCTCTCCAG 20

RESULT 177
I25690 20 bp DNA linear PAT 07-OCT-1996
LOCUS Sequence 9 from patent US 5552283.
DEFINITION I25690
ACCESSION I25690
VERSION I25690.1 GI:1605560
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.
TITLE Method, reagents and kit for diagnosis and targeted screening for
p53 mutations
JOURNAL Patent: US 5552283-A 9 03-SEP-1996;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
DB 18 TCGTCTCTCCAG 7

RESULT 178
I43305 20 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 123 from patent US 5631146.
DEFINITION I43305
ACCESSION I43305
VERSION I43305.1 GI:2468549
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Scotrak,J.W. and Huizenga,D.E.
TITLE DNA aptamers and catalysts that bind adenosine or
adenosine-5'-phosphates and methods for isolation thereof
JOURNAL Patent: US 5631146-A 123 20-MAY-1997;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCCTCCGCTA 191
DB 16 CTTCCTCCGCTA 5

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RESULT 179
AR206720      20 bp   DNA      linear   PAT 20-JUN-2002
LOCUS        Sequence 1 from patent US 6372436.
DEFINITION   AR206720
ACCESSION    AR206720
VERSION      AR206720.1 GI:21505407
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Pouzyrev,A.,Timofeyevich, and Riddle,D.Iee.
TITLE       Method for construction of cDNA libraries enriched in clones
            corresponding to rare mRNA
JOURNAL      Patent: US 6372436-A 1 16-APR-2002;
FEATURES
SOURCE       1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CCGCTGGAGCCC 257
Db 1 CTCCTGGAGCCC 12

RESULT 180
AR265991      20 bp   DNA      linear   PAT 10-APR-2003
LOCUS        Sequence 172 from patent US 6492170.
DEFINITION   AR265991
ACCESSION    AR265991
VERSION      AR265991.1 GI:29694837
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Watt,A.T.
TITLE       Antisense modulation of caspase 9 expression
JOURNAL      Patent: US 6492170-A 172 10-DEC-2002;
FEATURES
SOURCE       1..20
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCGGAGGAGGTT 32
Db 5 CCGGAGGAGGTT 16

RESULT 181
AR281883      20 bp   DNA      linear   PAT 10-APR-2003
LOCUS        Sequence 6 from patent US 6521407.
DEFINITION   AR281883
ACCESSION    AR281883
VERSION      AR281883.1 GI:29717811
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Warentz,H.M. and Seabra,L.A.
TITLE       Methods for determining chemosensitivity of cancer cells based upon
            expression of negative and positive signal transduction factors

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JOURNAL      Patent: US 6521407-A 6 18-FEB-2003;
FEATURES
SOURCE       1..20
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20

RESULT 182
AR299997      20 bp   DNA      linear   PAT 12-JUN-2003
LOCUS        Sequence 11732 from patent US 6537751.
DEFINITION   AR299997
ACCESSION    AR299997
VERSION      AR299997.1 GI:31687281
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 11732 25-MAR-2003;
FEATURES
SOURCE       1..20
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 511 CGTCTCTCCAGA 522
Db 14 CGTCTCTCCAGA 3

RESULT 183
AR310801      20 bp   DNA      linear   PAT 12-JUN-2003
LOCUS        Sequence 1338 from patent US 6559294.
DEFINITION   AR310801
ACCESSION    AR310801
VERSION      AR310801.1 GI:31704227
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Griffiths,R., Hoiseeth,S.K., Zagursky,R.J., Metcalfe,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
TITLE       Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 1338 06-MAY-2003;
FEATURES
SOURCE       1..20
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 CTGAGATCTTC 327

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Db 9 CTGAGGATCTTC 20

RESULT 184  
AR337679  
LOCUS AR337679 20 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 14 from patent US 6566514.  
ACCESSION AR337679  
VERSION AR337679.1 GI:33724247  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS 1 (bases 1 to 20)  
TITLE Wright, J.A., Young, A.H. and Lee, Y.S.  
Oligonucleotide sequences complementary to thioredoxin or  
thioredoxin reductase genes and methods of using same to modulate  
cell growth  
JOURNAL Patent: US 6566514-A 14 20-MAY-2003;  
FEATURES  
LOCATION/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 442 TCGAATCTTT 453  
Db 7 TCGAATCTTT 18

RESULT 185  
AR432224  
LOCUS AR432224 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 21 from patent US 6653133.  
ACCESSION AR432224  
VERSION AR432224.1 GI:40194497  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS 1 (bases 1 to 20)  
TITLE Dean, N.M., Marcusson, E.G. and Wyatt, J.  
Antisense modulation of Fas mediated signaling  
JOURNAL Patent: US 6653133-A 21 25-NOV-2003;  
FEATURES  
LOCATION/Qualifiers  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 GGAATGCTCTT 182  
Db 20 GGAATGCTCTT 9

RESULT 186  
AR437041  
LOCUS AR437041 20 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 93 from patent US 6656732.  
ACCESSION AR437041  
VERSION AR437041.1 GI:40200125  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Bennett, C.F. and Watt, A.T.  
TITLE Antisense inhibition of src-c expression  
JOURNAL Patent: US 6656732-A 93 02-DEC-2003;  
FEATURES  
source 1..20  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 280 GTGGCCGACTTT 291  
Db 15 GTGGCCGACTTT 4

RESULT 187  
AX018874  
LOCUS AX018874 20 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 6 from Patent WO942839.  
ACCESSION AX018874  
VERSION AX018874.1 GI:10042970  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE  
AUTHORS 1  
TITLE Warentius, H.  
JOURNAL Treating cancer  
THERYTE LIMITED (GB); WARENTIUS HILMAR (GB)  
Patent: WO 942839-A 6 26-AUG-1999;  
FEATURES  
LOCATION/Qualifiers  
source 1..20  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 TCCTCTCTCCAG 521  
Db 9 TCCTCTCTCCAG 20

RESULT 188  
AX018889  
LOCUS AX018889 20 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 6 from Patent WO942834.  
ACCESSION AX018889  
VERSION AX018889.1 GI:10042985  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM artificial sequences.

REFERENCE  
AUTHORS 1  
TITLE Seabra, L.A. and Warentius, H.  
JOURNAL Treating cancer  
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENTIUS HILMAR (GB)  
Patent: WO 942834-A 6 26-AUG-1999;  
FEATURES  
LOCATION/Qualifiers  
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/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="PRIMER"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 510 TCCTCTCTCCAG 521  
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 DB 9 TCCTCTCTCCAG 20

## RESULT 189

AX018906 20 bp DNA linear PAT 07-SEP-2000  
 LOCUS AX018906 Sequence 6 from Patent WO9942828.  
 ACCESSION AX018906  
 VERSION AX018906.1 GI:10043000  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Warenus, H.M.  
 TITLE Treating cancer  
 JOURNAL Patent: WO 9942828-A 6 26-AUG-1999;  
 THERYTE LIMITED (GB); WARENUS HILMAR MEEK (GB)  
 Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PRIMER"

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Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 510 TCCTCTCTCCAG 521  
 |||||  
 DB 9 TCCTCTCTCCAG 20

## RESULT 190

AX018921 20 bp DNA linear PAT 07-SEP-2000  
 LOCUS AX018921 Sequence 6 from Patent WO9942821.  
 ACCESSION AX018921  
 VERSION AX018921.1 GI:10043016  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.  
 REFERENCE 1  
 AUTHORS Seabra, L.A. and Warenus, H.M.  
 TITLE Treating cancer  
 JOURNAL Patent: WO 9942821-A 6 26-AUG-1999;  
 SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENUS HILMAR MEEK (GB)  
 Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PRIMER"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 510 TCCTCTCTCCAG 521  
 |||||

DB 9 TCCTCTCTCCAG 20

RESULT 191 20 bp DNA linear PAT 07-SEP-2000  
 AX019035  
 LOCUS AX019035 Sequence 6 from Patent WO9942090.  
 ACCESSION AX019035  
 VERSION AX019035.1 GI:10043116  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Warenus, H.M.  
 TITLE Treating cancer  
 JOURNAL Patent: WO 9942090-A 6 26-AUG-1999;  
 THERYTE LIMITED (GB); WARENUS HILMAR MEEK (GB)  
 Location/Qualifiers  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="PRIMER"

## ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 510 TCCTCTCTCCAG 521  
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 DB 9 TCCTCTCTCCAG 20

## RESULT 192

AX293651 20 bp DNA linear PAT 21-NOV-2001  
 LOCUS AX293651 Sequence 5413 from Patent WO0179548.  
 ACCESSION AX293651  
 VERSION AX293651.1 GI:1705334  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1  
 AUTHORS Barany, F., Zivri, M., Gerry, N.P., Favis, R. and Kliman, R.  
 TITLE Method of designing addressable array for detection of nucleic acid  
 JOURNAL sequence differences using ligase detection reaction  
 Patent: WO 0179548-A 5413-25-OCT-2001;  
 CORNELL RESEARCH FOUNDATION, INC. (US)  
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 DB 9 ACCTACCTGTGC 20

RESULT 193 20 bp DNA linear PAT 21-NOV-2001  
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 ACCESSION AX293867

VERSION AX293867.1 GI:17055550  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
ARTIFICIAL SEQUENCES.  
REFERENCE 1  
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 529 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
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QY 52 GTCCGCTG3GCT 63  
DB 12 GTCCGCTG3GCT 1  
RESULT 194  
AX295341/c AX295341 20 bp DNA linear PAT 21-NOV-2001  
LOCUS Sequence 7103 from Patent WO0179548.  
DEFINITION  
ACCESSION AX295341  
VERSION AX295341.1 GI:17057030  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
ARTIFICIAL SEQUENCES.  
REFERENCE 1  
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.  
TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 7103 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 154 AAGACGCGCTGC 165  
DB 19 AAGACGCGCTGC 8  
RESULT 195  
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LOCUS Sequence 8803 from Patent WO0179548.  
DEFINITION  
ACCESSION AX297041  
VERSION AX297041.1 GI:17058732  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
ARTIFICIAL SEQUENCES.  
REFERENCE 1  
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.

TITLE Method of designing addressable array for detection of nucleic acid  
JOURNAL sequence differences using ligase detection reaction  
PATENT: WO 0179548-A 8803 25-OCT-2001;  
CORNELL RESEARCH FOUNDATION, INC. (US)  
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QY 584 CTTGGGACTTT 595  
DB 20 CTTGGGACTTT 9  
RESULT 196  
AX301845 AX301845 20 bp DNA linear PAT 30-NOV-2001  
LOCUS Sequence 6 from Patent WO0185917.  
DEFINITION  
ACCESSION AX301845  
VERSION AX301845.1 GI:17382902  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
ARTIFICIAL SEQUENCES.  
REFERENCE 1  
AUTHORS Abduljadayel,I.M.  
TITLE A device  
JOURNAL Patent: WO 0185917-A 6 15-NOV-2001;  
Tristem Ireland Limited (IE)  
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QY 317 TGAGATCTTCA 328  
DB 5 TGAGATCTTCA 16  
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AX459997 AX459997 20 bp DNA linear PAT 08-JUL-2002  
LOCUS Sequence 8 from Patent WO0203849.  
DEFINITION  
ACCESSION AX459997  
VERSION AX459997.1 GI:21725730  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Schena,M.A.  
TITLE Microarray method of genotyping multiple samples at multiple loci  
JOURNAL Patent: WO 0203849-A 8 17-JUN-2002;  
Telechem International, Inc. (US)  
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7 CTGAGAGCCCGCTG 18
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RESULT 198
AX613711 20 bp DNA linear PAT 17-FEB-2003
DEFINITION Sequence 4736 from Patent WO02072882.
ACCESSION AX613711
VERSION AX613711.1 GI:28409140
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Cullen, P. and Seedorf, U.
AUTHORS Coronary chip
JOURNAL Patent: WO 02072882-A 4736 19-SEP-2002;
OGHAM GmbH (DE)
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QY 161 GCTGCCACGCTG 172
2 GCTGCCACGCTG 13
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RESULT 199
AX710965 20 bp RNA linear PAT 11-APR-2003
LOCUS AX710965
DEFINITION Sequence 265 from Patent EP1288296.
ACCESSION AX710965
VERSION AX710965.1 GI:29787346
KEYWORDS
SOURCE Human herpesvirus 5
ORGANISM Human herpesvirus 5
Virus; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
REFERENCE
1 Draper, K.G., McSwigen, J.A., Holecsek, J.J., Dudycz, L.W.,
AUTHORS Macejak, D.G. and Mamone, J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 265 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
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QY 223 TGCTACCGCGTC 234
Db 4 TGCTACCGCGTC 15

RESULT 200
BD001106 20 bp RNA linear PAT 31-JAN-2002
LOCUS BD001106
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001106
VERSION BD001106.1 GI:18625665
KEYWORDS UP 2000342285-A/266.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Draper, K.G., Dadykiz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holecsek, J.J., and Mamone, J.A.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 266 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342285-A/266
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132616
PF 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882866, 14-MAY-1992 US 07/882868 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884433 PR
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14-MAY-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22//C12N5/10, C12R1:91, PC
C12N15/00
PC C12N5/00, C12N5/00, C12R1:91
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 223 TGCTACCGCGTC 234
4 TGCTACCGCGTC 15
Db

RESULT 201
BD001535 20 bp RNA linear PAT 31-JAN-2002
LOCUS BD001535
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001535
VERSION BD001535.1 GI:18626094
KEYWORDS UP 2000342286-A/266.

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SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.

REFERENCE  
1 (bases 1 to 20)

AUTHORS  
Draper, R.G., Dadykiz, J.W., Macswigen, J.A., Mayesjak, D.G.,  
Holesek, J.J., and Mamone, A.J.

TITLE  
Method and reagent for inhibiting viral replication

JOURNAL  
Patent: JP 2000342286-A 266 12-DEC-2000;  
RIBOZYME PHARMACEUTICALS INC

COMMENT  
OS Artificial Sequence  
PN JP 2000342286-A/266  
PD 12-DEC-2000  
PR 01-MAY-2000 JP 2000332651  
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR  
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR  
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR  
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR  
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR  
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR  
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR  
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR  
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR  
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR  
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR  
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR  
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR  
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PR  
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G  
MAYESJAK, PI  
PI JAMES J HOLESEK, ANTHONY J MAMONE  
PC C12N15/09, C12N15/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,  
PC A61K39/135,  
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K46/00,  
PC A61P1/16,  
PC A61P3/14, A61P3/15, A61P3/18, A61P3/22, A61P35/02, C12Q1/68, PC  
(C12N15/09, C12R1/93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC  
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DB 4 TCTTACCGCGTC 15

RESULT 202  
BD071075 20 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.  
ACCESSION BD071075  
VERSION BD071075.1 GI:22616678  
KEYWORDS JP 2001517929-A/41.  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
1 (bases 1 to 20)  
REFERENCE  
AUTHORS Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C.  
TITLES Modulation of mammalian telomerase by peptide nucleic acids  
JOURNAL Patent: JP 2001517929-A 41 09-OCT-2001;  
GERON CORP  
COMMENT OS Unidentified

PN JP 2001517929-A/41  
PD 09-OCT-2001  
PR 09-APR-1997 JP 1997536487  
PR 09-APR-1996 US 08/630019  
PI JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID  
PI COREY, C  
PI JAMES C NORTON  
PC C07K14/00, A61K38/16, C12Q1/68  
CC Strandedness: Single;  
CC Topology: Linear;  
CC /desc = 'peptide nucleic acid (PNA), where (deoxy)ribose-CC  
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DB 1 AGATCTTCAC 12

RESULT 203  
BD071080 20 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION Modulation of mammalian telomerase by peptide nucleic acids.  
ACCESSION BD071080  
VERSION BD071080.1 GI:22616683  
KEYWORDS JP 2001517929-A/46.  
SOURCE unidentified  
ORGANISM unidentified  
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1 (bases 1 to 20)  
REFERENCE  
AUTHORS Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C.  
TITLES Modulation of mammalian telomerase by peptide nucleic acids  
JOURNAL Patent: JP 2001517929-A 46 09-OCT-2001;  
GERON CORP  
COMMENT OS Unidentified  
PN JP 2001517929-A/46  
PD 09-OCT-2001  
PR 09-APR-1997 JP 1997536487  
PR 09-APR-1996 US 08/630019  
PI JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID  
PI COREY, C  
PI JAMES C NORTON  
PC C07K14/00, A61K38/16, C12Q1/68  
CC Strandedness: Single;  
CC Topology: Linear;  
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Db	1	AGGATCTTCACC	12

LOCUS	DEFINITION	ACCESION	FEATURES	COMMENT
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synthetic construct	artificial sequences.	1 (bases 1 to 20)

JOURNAL  
Patent: JP 2001321190-A 687 20-NOV-2001;  
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA  
GENOTECHS  
OS Artificial Sequence  
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RESULT 205  
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RESULT 206
BD131952
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cell proliferation.  
BD131952  
BD131952.1 GI:23226897  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 20)  
REFERENCE  
Wardle, J. A., Young, J. H., and Fox, V. C.  
NUMBERS

JOURNAL  
Patent: JP 2002501743-A 14 22-JAN-2002;  
GENESENE TECHNOLOGIES INC  
OS Homo sapiens (human)  
PM ID 2002501743-2/14  
COMMENT

PF 29-JAN-1999 JP 2000529423  
PR 30-JAN-1998 US 60/073196  
PI JIM A WRIGHT, AIPING H YOUNG, YOON S LEE  
PC A61K15/09, A61K13/711, A61K46/00, A61P35/00, A61P35/04, C07H21/04///  
PC A61K13/711, A61K45/00, A61K46/00, A61P35/00, C12N5/00 CC

CC	reducease gene and utilization thereof for controlling cell
CC	proliferation
CC	location/Qualifiers
FH	Key
FT	source
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Matches 12; Conservative 0; Mismatches 0; Gaps 0;

COMMENT	OS	Artificial Sequence
	PN	JP 2001321190-A/1423
	PD	20-NOV-2001
	PF	12-MAR-2001 JP 2001066285
	PI	ETICH SOEDA

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RESULT 207
BD135497/c      20 bp   DNA      linear   PAT 18-SEP-2002
LOCUS           BD135497
DEFINITION      Methods for analyzing animal products.
ACCESSION       BD135497
VERSION         BD135497.1 GI:23230442
KEYWORDS        JP 2002504814-A/35.
SOURCE          unidentified
ORGANISM        unidentified
REFERENCE       1 (bases 1 to 20)
AUTHORS         Anderson,L., Kijss,J., Giuffra,E., Jon,G., Evans,R. and
                Plascow,G.S.
TITLE           Methods for analyzing animal products
JOURNAL         Patent: JP 2002504814-A 35 12-FEB-2002;
                PIG IMPROVEMENT CO UK LTD
COMMENT         OS Unidentified
                PN JP 2002504814-A/35
                PD 12-FEB-2002
                PF 27-MAY-1998 JP 1999500368
                PR 30-MAY-1997 GB 9711214.8,31-JAN-1998 GB 9801990.4 PI
                LEIF ANDERSSON,JAMES KIJSS,ELISABETTA GIUFFRA,GARY JON PI
                EVANS,RICHARD WALES.
                PI GRAHAM STUART PLASTOW
                PC C12Q1/68
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Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 243 CACCTCCTGGAG 254
DB 20 CACCTCCTGGAG 9
RESULT 208
BD170190
LOCUS           BD170190
DEFINITION      Method of synthesizing single-stranded nucleic acid.
ACCESSION       BD170190
VERSION         BD170190.1 GI:27876002
KEYWORDS        WO 0234907-A/22.
SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE       1 (bases 1 to 20)
AUTHORS         Nagamine,K., Hase,T. and Notomi,T.
TITLE           Method of synthesizing single-stranded nucleic acid
JOURNAL         Patent: WO 0234907-A 22 02-MAY-2002;
                BIKEN CHEMICAL CO LTD,KENTARO NAGAMINE,TETSU HASE,TSUGUNORI NOTOMI
COMMENT         OS Artificial Sequence
                PN WO 0234907-A/22
                PD 02-MAY-2002
                PF 26-OCT-2001 WO 2001JP009452
                PR 27-OCT-2000 JP 00P 328219
                PI KENTARO NAGAMINE,TETSU HASE,TSUGUNORI NOTOMI
                PC C12N15/10,C12Q1/68
                CC Description of Artificial Sequence:Outer primer(Forward) FH
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Query Match    2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 319 AGGATCTTCACC 330
DB 7 AGGATCTTCACC 18
RESULT 209
AB068586
LOCUS           AB068586
DEFINITION      Synthetic construct DNA, forward primer for human STS-R90NSR at
                1p36.
ACCESSION       AB068586
VERSION         AB068586.1 GI:15129390
KEYWORDS
SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE       1
AUTHORS         Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
                Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
                Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
                and Soeda,E.
TITLE           A BAC-based STS-content map spanning a 35-Mb region of human
                chromosome 1p35-p36
JOURNAL         Genomics 74 (1), 55-70 (2001)
MEDLINE         21269192
PUBMED          11374902
REFERENCE       2 (bases 1 to 20)
AUTHORS         Horii,A.
TITLE           Direct Submission
JOURNAL         Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
                Medicine, Molecular Pathology/2-1 Setiyomachi, Aoba-ku, Sendai,
                Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
                Tel:81-22-717-8042 Fax:81-22-717-8047)
FEATURES
source          Location/Qualifiers
                1..20
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"
                1..20
                /note="forward primer for human STS sts-R90NSR at 1p36
                sts-R90NSR obtained from clones B133N1, B369A24, B341F17,
                B262P12, B341F17, B334L24, B12802, B90N5, B229F2, Human
                BAC library RPCI-11"
ORIGIN
Query Match    2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 494 TGCATGAAATTT 505
DB 8 TGCATGAAATTT 19
RESULT 210
AB069312/c
LOCUS           AB069312
DEFINITION      Synthetic construct DNA, forward primer for human STS-stsG1j123
                at 1p36.
ACCESSION       AB069312
VERSION         AB069312.1 GI:15130116
KEYWORDS

```

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Matsubae, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, N., Horii, A.
            and Soeda, E.
TITLE       A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
JOURNAL     Genomics 74 (1), 55-70 (2001)
MEDLINE    2126192
PUBMED     11374902
REFERENCE   2 (bases 1 to 20)
AUTHORS     Horii, A.
TITLE       Direct Submission
JOURNAL     Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES   1..20
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            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
            misc_feature
            1..20
            /note="forward primer for human STS sts-stsG3123 at 1p36
            sts-stsG3123 obtained from clones B157K6, B14F15, B21G9,
            B21F9, Human BAC library Rpci-11"

ORIGIN
Query Match      2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      338 TCTACTTCTGTG 349
        |||||
        12 TCTACTTCTGTG 1

RESULT 211
AX627549      11 bp      DNA      linear      PAT 24-FEB-2003
LOCUS         AX627549
DEFINITION    Sequence 4590 from Patent WO02053774.
ACCESSION     AX627549
VERSION       AX627549.1 GI:28455587
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4590 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     1..11
            Location/Qualifiers
            source
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      569 GAGACGATTT 579
        |||||
        1 GAGACGATTT 11

RESULT 212

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AX628350/c    11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS         AX628350
DEFINITION    Sequence 5391 from Patent WO02053774.
ACCESSION     AX628350
VERSION       AX628350.1 GI:28456388
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5391 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     1..11
            Location/Qualifiers
            source
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCGTGAGGCC 257
        |||||
        11 TCGTGAGGCC 1

RESULT 213
AX629660      11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS         AX629660
DEFINITION    Sequence 6701 from Patent WO02053774.
ACCESSION     AX629660
VERSION       AX629660.1 GI:28457698
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE     1
AUTHORS      Petersohn, D., Conrad, M. and Hofmann, K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6701 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     1..11
            Location/Qualifiers
            source
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      445 AATACCTTTGT 455
        |||||
        1 AATACCTTTGT 11

RESULT 214
AX632806      11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS         AX632806
DEFINITION    Sequence 9848 from Patent WO02053774.
ACCESSION     AX632806
VERSION       AX632806.1 GI:28468421
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1  
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.  
TITLE Method for determining homeostasis of the skin  
JOURNAL Patent: WO 02053774-A 9848 11-JUL-2002;  
Henkel Kommanditgesellschaft auf Aktien (DE)  
FEATURES Location/Qualifiers  
source 1..11  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 480 AGCCTGGAG 490  
DB 1 AGCCTGGAG 11  
RESULT 215  
LOCUS AR058692 12 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 269 from patent US 5837832.  
ACCESSION AR058692  
VERSION AR058692.1 GI:5984269  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 12)  
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,  
Lipshutz,R.J., Lohman,P.E., Morris,M.S. and Sheldon,B.L.  
TITLE Arrays of nucleic acid probes on biological chips  
JOURNAL Patent: US 5837832-A 269 17-NOV-1998;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 462 CCATGAAGA 472  
DB 2 CCATGAAGA 12  
RESULT 216  
LOCUS BD242529 12 bp DNA linear PAT 17-JUL-2003  
DEFINITION A system for cell based screening.  
ACCESSION BD242529  
VERSION BD242529.1 GI:33052299  
KEYWORDS JP 2002528136-A/35.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.  
TITLE A system for cell based screening  
JOURNAL Patent: JP 2002528136-A 35 03-SEP-2002;  
CELLONICS INC  
OS Artificial Sequence  
PN JP 2002528136-A/35  
PD 03-SEP-2002  
PR 29-OCT-1999 JP 2000579780  
PR 30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI  
KENNETH A.GUILIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI

TENCZA  
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/  
PC 37,G01N33/15,  
PC G01N33/50,C12N15/00,C12N5/00  
CC Description of Artificial Sequence: proCaspase-6 substrate CC  
recognition  
CC sequence  
FH Key Location/Qualifiers  
FT source 1..12  
FT /organism='Artificial Sequence'.  
FEATURES  
source 1..12  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 338 TCTACTTCTGT 348  
DB 11 TCTACTTCTGT 1  
RESULT 217  
LOCUS AR217454 12 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 69 from patent US 6416959.  
ACCESSION AR217454  
VERSION AR217454.1 GI:23317147  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 12)  
AUTHORS Guiliano,K. and Kapur,R.  
TITLE System for cell-based screening  
JOURNAL Patent: US 6416959-A 69 09-JUL-2002;  
FEATURES Location/Qualifiers  
source 1..12  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 338 TCTACTTCTGT 348  
DB 11 TCTACTTCTGT 1  
RESULT 218  
LOCUS AX766780 12 bp DNA linear PAT 25-JUN-2003  
DEFINITION Sequence 69 from Patent EP1314980.  
ACCESSION AX766780  
VERSION AX766780.1 GI:32260534  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Guiliano,K.A. and Kapur,R.  
TITLE A system for cell-based screening  
JOURNAL Patent: EP 1314980-A 69 28-MAY-2003;  
CELLONICS, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..12  
/organism="synthetic construct"

ORIGIN /mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="proCaspase-6 substrate recognition sequence"

Query Match 1.8%; Score 11; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTTCTGT 348  
|||||  
11 TCTACTTCTGT 1

Db 11 TCTACTTCTGT 1

RESULT 219  
LOCUS AX555912 13 bp DNA linear PAT 27-NOV-2002  
DEFINITION Sequence 508 from Patent WO02070755.  
ACCESSION AX555912  
VERSION AX555912.1 GI:25899370  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Lyamichay,V.I., Kaiser,M.W. and Lyamichaya,N.  
TITLE Pen endonucleases  
JOURNAL Patent: WO 02070755-A 508 12-SEP-2002;  
Third Wave Technologies, Inc. (US)  
Location/Qualifiers

FEATURES  
source 1.13  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 AGAGGCGGTGAC 111  
|||||  
Db 13 AGAGGCGGTGAC 3

RESULT 220  
LOCUS AJ598336 13 bp DNA linear PLN 23-OCT-2003  
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 466D02.  
ACCESSION AJ598336  
VERSION AJ598336.1 GI:37947964  
KEYWORDS right border; T-DNA flanking sequence.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE 1  
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepointec,L., Caboche,M. and Lecharny,A.  
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
PUBMED 12445565  
REFERENCE 2 (bases 1 to 13)  
AUTHORS Balzergue,S.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMGCV, INRA/CNRS. 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.inbioigen.fr>).

FEATURES  
source 1.13  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultiivar="Massillewskija"  
/db\_xref="taxon:3702"  
/clone="466D02"  
/clone\_1lb="Arabidopsis thaliana T-DNA insertion lines"  
1.13  
/note="T-DNA flanking sequence  
right border"

ORIGIN

Query Match 1.8%; Score 11; DB 8; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 AAAGATTATT 434  
|||||  
Db 3 AAAGATTATT 13

RESULT 221  
LOCUS A42580 14 bp DNA linear PAT 06-MAR-1997  
DEFINITION Sequence 97 from Patent WO9502051.  
ACCESSION A42580  
VERSION A42580.1 GI:2298029  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.  
TITLE A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS  
JOURNAL Patent: WO 9502051-A 97 19-JAN-1995;  
BIOGEN/STIK GES FUER BIOMOLEKUL (DB)  
COMMENT Other publication AU 7345694 950206.  
Location/Qualifiers

FEATURES  
source 1.14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 TCATGACCTTC 423  
|||||  
Db 2 TCATGACCTTC 12

RESULT 222  
LOCUS A88769 14 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 917 from Patent WO9833904.  
ACCESSION A88769  
VERSION A88769.1 GI:6737339

KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Brysch, W. and Schlingensiepen, K.  
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD  
JOURNAL Patent: WO 9833904-A 917 06-AUG-1998;  
BIOGENOSITIK GES. (DE); BRYSCH WOLFGANG (DE)  
FEATURES  
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1. .14  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 413 TCATGACCTTC 423  
DB 2 TCATGACCTTC 12  
RESULT 223  
188009 14 bp DNA linear PAT 10-AUG-1998  
LOCUS  
DEFINITION Sequence 1 from patent US 5716835.  
ACCESSION 188009  
VERSION 188009.1 GI:3407949  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Regan, C.W., Gil, D.W. and Woodward, D.F.  
TITLE Nucleic acid encoding a novel human EP prostaglandin receptor  
JOURNAL Patent: US 5716835-A 1 10-FEB-1998;  
FEATURES  
source  
1. .14  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGGAGCC 256  
DB 3 CTCCTGGAGCC 13  
RESULT 224  
AR372103 14 bp DNA linear PAT 12-SEP-2003  
LOCUS  
DEFINITION AR372103 Sequence 1 from patent US 6395878.  
ACCESSION AR372103  
VERSION AR372103.1 GI:34609385  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Regan, C.W., Gil, D.W. and Woodward, D.F.  
TITLE Nucleic acid encoding a human EP prostaglandin receptor  
JOURNAL Patent: US 6395878-A 1 28-MAY-2002;  
FEATURES  
source  
1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 246 CTCCTGGAGCC 256  
DB 3 CTCCTGGAGCC 13  
RESULT 225  
AX133710/c 14 bp DNA linear PAT 15-MAY-2001  
LOCUS  
DEFINITION AX133710 Sequence 8 from Patent WO0130381.  
ACCESSION AX133710  
VERSION AX133710.1 GI:14139720  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS Abarinejad, S.  
TITLE Use of csf-1 inhibitors  
JOURNAL Patent: WO 0130381-A 8 03-MAY-2001;  
Hofbauer, Reinhold (AT)  
FEATURES  
source  
1. .14  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 389 ACCGCGCCGGG 399  
DB 12 ACCGCGCCGGG 2  
RESULT 226  
BD066282 14 bp DNA linear PAT 27-AUG-2002  
LOCUS  
DEFINITION BD066282 An antisense oligonucleotide preparation method.  
ACCESSION BD066282  
VERSION BD066282.1 GI:22611885  
KEYWORDS JP 2001511000-A/917.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
1 (bases 1 to 14)  
AUTHORS Schlingensiepen, K.H. and Brysch, W.  
TITLE An antisense oligonucleotide preparation method  
JOURNAL Patent: JP 2001511000-A 917 07-AUG-2001;  
BIOGENOSITIK GESELLSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH  
COMMENT  
OS Unknown  
PN JP 2001511000-A/917  
PD 07-AUG-2001  
PF 30-JAN-1998 JP 199853253  
PR 31-JAN-1997 EP 97101311.8  
PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH  
PC C12N15/11, C07H21/04, A61K31/70  
CC An antisense oligonucleotide preparation method FH Key  
FEATURES  
source  
1. .14  
/organism="unknown"  
Location/Qualifiers  
1. .14  
/organism="unknown"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 TCATGACCTTC 423  
DB 2 TCATGACCTTC 12

RESULT 227  
BD201796 14 bp RNA linear PAT 17-JUL-2003  
LOCUS Method and reagent for treating diseases or conditions concerning  
DEFINITION molecule participating in vasculogenic response.  
ACCESSION BD201796.1 GI:33011566  
VERSION BD201796.1  
KEYWORDS JP 2002509721-A/4822.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
TITLES 1 (bases 1 to 14)  
Pavco, P.A., Roberts, E., Jarvis, T., Coesholt, C. and Mcswigen, J.A.  
Method and reagent for treating diseases or conditions concerning  
molecule participating in vasculogenic response  
Patent: JP 2002509721-A 4822 02-APR-2002;  
RIBOZYME PHARMACEUTICALS INC

COMMENT  
OS Homo sapiens (human)  
PN JP 2002509721-A/4822  
PD 02-APR-2002  
PF 24-MAR-1998 JP 2000541291  
PR 27-MAR-1998 US 60/079678  
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,  
PI JAMES A MCSWIGEN

FEATURES  
source  
CC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC  
A61P29/00  
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC  
C12N5/00  
CC Method and reagent for treating diseases or conditions CC  
concerning molecule  
CC participating in vasculogenic response  
FH Key Location/Qualifiers  
FT source 1..14  
FT Location/Qualifiers  
1..14  
/organism="Homo sapiens (human)"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:9606"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 GCTGCTACCGC 231  
DB 13 GCTGCTACCGC 3

RESULT 228  
BD209325 14 bp RNA linear PAT 17-JUL-2003  
LOCUS Enzymatic nucleic acid treatment of diseases or conditions related  
DEFINITION to hepatitis C virus infection.  
ACCESSION BD209325  
VERSION BD209325.1 GI:33019095  
KEYWORDS JP 2002512791-A/2915.  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE  
AUTHORS unclassified.  
TITLES 1 (bases 1 to 14)  
Blatt, L., Mcswigen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.  
Enzymatic nucleic acid treatment of diseases or conditions related  
to hepatitis C virus infection  
Patent: JP 2002512791-A 2915 08-MAY-2002;  
RIBOZYME PHARMACEUTICALS INC

COMMENT  
OS Hepatitis virus (hepatitis C virus)  
PN JP 2002512791-A/2915  
PD 08-MAY-2002  
PF 26-APR-1998 JP 2000545991  
PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR  
25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI  
LAWRENCE BLATT, JAMES A MCSWIGEN, ELISABETH ROBERTS, PAMELA A PI  
PAVCO.

PI DENNIS MACEJAK  
PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P11/12, C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions CC  
related to  
CC hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1..14  
FT Location/Qualifiers  
1..14  
/organism="Hepatitis virus (hepatitis C FT  
virus)"  
/organism="unidentified"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:32644"

FEATURES  
source  
CC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P11/12, C12N15/09,  
PC A61K37/66,  
PC C12N15/00  
CC Enzymatic nucleic acid treatment of diseases or conditions CC  
related to  
CC hepatitis C virus infection.  
FH Key Location/Qualifiers  
FT source 1..14  
FT Location/Qualifiers  
1..14  
/organism="Hepatitis virus (hepatitis C FT  
virus)"  
/organism="unidentified"  
/mol\_type="genomic RNA"  
/db\_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 TGGCCGCTGCT 226  
DB 1 TGGCCGCTGCT 11

RESULT 229  
AR033266/c 15 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 32 from patent US 5869253.  
DEFINITION AR033266  
ACCESSION AR033266  
VERSION AR033266.1 GI:5948871  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 15)  
Draper, K.G.  
TITLES Method and reagent for inhibiting hepatitis C virus replication  
JOURNAL Patent: US 5869253-A 32 09-FEB-1999;  
FEATURES Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
DB 13 AGGCTGAGCCC 3

RESULT 230  
AR056295

LOCUS AR056295 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 499 from patent US 5837542.  
 ACCESSION AR056295  
 VERSION AR056295.1 GI:5961872  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 499 17-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
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 4 ACCTCCTGGAG 14

Db

RESULT 231  
 LOCUS AR056484 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 688 from patent US 5837542.  
 ACCESSION AR056484  
 VERSION AR056484.1 GI:5982061  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 688 17-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
 |||||  
 4 ACCTCCTGGAG 14

Db

RESULT 232  
 LOCUS AR056532 15 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 736 from patent US 5837542.  
 ACCESSION AR056532  
 VERSION AR056532.1 GI:5982109  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 736 17-NOV-1998;

FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
 |||||  
 4 ACCTCCTGGAG 14

Db

RESULT 233  
 LOCUS AR071434 15 bp DNA linear PAT 18-FEB-2000  
 DEFINITION Sequence 31 from patent US 5910626.  
 ACCESSION AR071434  
 VERSION AR071434.1 GI:7222322  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Haselkorn,R. and Gornicki,P.  
 TITLE Acetyl-CoA carboxylase compositions and methods of use  
 JOURNAL Patent: US 5910626-A 31 08-JUN-1999;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 555 GGTTGATGACT 565  
 |||||  
 4 GGTTGATGACT 14

Db

RESULT 234  
 LOCUS AR113088/c 15 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 32 from patent US 6132966.  
 ACCESSION AR113088  
 VERSION AR113088.1 GI:14093410  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Draper,K.G.  
 TITLE Method and reagent for inhibiting hepatitis C virus replication  
 JOURNAL Patent: US 6132966-A 32 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..15  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369  
 |||||  
 13 AGGCTGAGCCC 3

Db

RESULT 235  
LOCUS ARI14053 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 499 from patent US 6132967.  
ACCESSION ARI14053  
VERSION ARI14053.1 GI:114094375  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 499 17-OCT-2000;  
FEATURES  
Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 244 ACCTCCTGGAG 254  
|||||  
4 ACCTCCTGGAG 14  
Db  
RESULT 236  
LOCUS ARI14242 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 688 from patent US 6132967.  
ACCESSION ARI14242  
VERSION ARI14242.1 GI:14094564  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 688 17-OCT-2000;  
FEATURES  
Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 244 ACCTCCTGGAG 254  
|||||  
4 ACCTCCTGGAG 14  
Db  
RESULT 237  
LOCUS ARI14290 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 736 from patent US 6132967.  
ACCESSION ARI14290  
VERSION ARI14290.1 GI:14094612  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 244 ACCTCCTGGAG 254  
|||||  
4 ACCTCCTGGAG 14  
Db

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 736 17-OCT-2000;  
FEATURES  
Location/Qualifiers  
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/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 244 ACCTCCTGGAG 254  
|||||  
4 ACCTCCTGGAG 14  
Db  
RESULT 238  
LOCUS ARI32197 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 622 from patent US 6194150.  
ACCESSION ARI32197  
VERSION ARI32197.1 GI:14121102  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 622 27-FEB-2001;  
FEATURES  
Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 418 ACCTCAAGG 428  
|||||  
4 ACCTCAAGG 14  
Db  
RESULT 239  
LOCUS ARI32198 15 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 623 from patent US 6194150.  
ACCESSION ARI32198  
VERSION ARI32198.1 GI:14121103  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 623 27-FEB-2001;  
FEATURES  
Location/Qualifiers  
1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred.No.3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 418 ACCTCAAGG 428  
|||||  
4 ACCTCAAGG 14  
Db

QY 418 ACCTCAAGA 428  
|||||  
Db 4 ACCTCAAGA 14

RESULT 240  
AR132199  
LOCUS Sequence 624 from patent US 6194150. 15 bp DNA  
DEFINITION AR132199  
ACCESSION AR132199.1 GI:14121104  
VERSION AR132199.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 624 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTCAAGA 428  
|||||  
Db 4 ACCTCAAGA 14

RESULT 241  
AR132200  
LOCUS Sequence 625 from patent US 6194150. 15 bp DNA  
DEFINITION AR132200  
ACCESSION AR132200.1 GI:14121105  
VERSION AR132200.1  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 625 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTCAAGA 428  
|||||  
Db 3 ACCTCAAGA 13

RESULT 242  
AR133396  
LOCUS Sequence 1821 from patent US 6194150. 15 bp DNA  
DEFINITION AR133396  
ACCESSION AR133396  
VERSION AR133396.1 GI:14122301  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 1821 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51  
|||||  
Db 5 AATTCAAAAT 15

RESULT 243  
AR133397  
LOCUS Sequence 1822 from patent US 6194150. 15 bp DNA  
DEFINITION AR133397  
ACCESSION AR133397  
VERSION AR133397.1 GI:14122302  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 1822 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51  
|||||  
Db 5 AATTCAAAAT 15

RESULT 244  
AR133398  
LOCUS Sequence 1823 from patent US 6194150. 15 bp DNA  
DEFINITION AR133398  
ACCESSION AR133398  
VERSION AR133398.1 GI:14122303  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 15)  
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.  
TITLE Nucleic acid based inhibition of CD40  
JOURNAL Patent: US 6194150-A 1823 27-FEB-2001;  
FEATURES Location/Qualifiers  
source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AATTCAAAAT 51  
|||||  
Db 5 AATTCAAAAT 15

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Db      5 AATTCAAAAAT 15
|||||
RESULT 245
LOCUS   I30019          15 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5578714.
ACCESSION I30019
VERSION   I30019.1      GI:1820810
KEYWORDS
SOURCE    Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Pogo,A.O. and Chaudhuri,A.
TITLE     DNA encoding Duffy ypd protein
JOURNAL   Patent: US 5578714-A 4 26-NOV-1996;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      477 CAAGCCTGGG 487
|||||
Db      15 CAAGCCTGGG 5
|||||

RESULT 246
LOCUS   I39402/c          15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 440 from patent US 5616488.
ACCESSION I39402
VERSION   I39402.1      GI:2083882
KEYWORDS
SOURCE    Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE     IL-5 targeted ribozymes
JOURNAL   Patent: US 5616488-A 440 01-APR-1997;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      441 CTGGAACTACTT 451
|||||
Db      12 CTGGAACTACTT 2
|||||

RESULT 247
LOCUS   I39403          15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 441 from patent US 5616488.
ACCESSION I39403
VERSION   I39403.1      GI:2083883
KEYWORDS
SOURCE    Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)

```

```

AUTHORS   Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE     IL-5 targeted ribozymes
JOURNAL   Patent: US 5616488-A 441 01-APR-1997;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      441 CTGGAACTACTT 451
|||||
Db      11 CTGGAACTACTT 1
|||||

RESULT 248
LOCUS   I39404/c          15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 442 from patent US 5616488.
ACCESSION I39404
VERSION   I39404.1      GI:2083884
KEYWORDS
SOURCE    Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE     IL-5 targeted ribozymes
JOURNAL   Patent: US 5616488-A 442 01-APR-1997;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      441 CTGGAACTACTT 451
|||||
Db      11 CTGGAACTACTT 1
|||||

RESULT 249
LOCUS   I57495/c          15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 32 from patent US 5610054.
ACCESSION I57495
VERSION   I57495.1      GI:2482559
KEYWORDS
SOURCE    Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Draper,K.G.
TITLE     Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL   Patent: US 5610054-A 32 11-MAR-1997;
FEATURES   Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      359 AGGCTGAGCCC 369
|||||

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Db 13 AGCGCTGAGCC 3

RESULT 250  
LOCUS 171878  
DEFINITION Sequence 4 from patent US 5683696.  
ACCESSION 171878  
VERSION 171878.1 GI:3008017  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Pogo, A., Oscar, and Chaudhuri, A.  
TITLE Cloning of Duffy blood group antigen, gpd  
JOURNAL Patent: US 5683696-A 4 04-NOV-1997,  
FEATURES Location/Qualifiers  
Source 1..15  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAAGCCTGGG 487  
Db 15 CAAAGCCTGGG 5

RESULT 251  
LOCUS AX133713 15 bp DNA  
DEFINITION Sequence 11 from Patent WO0130381.  
ACCESSION AX133713  
VERSION AX133713.1 GI:14139723  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Aharinejad, S.  
TITLE Use of csi-1 inhibitors  
JOURNAL Patent: WO 0130381-A 11 03-MAY-2001;  
Hofbauer, Reinhold (AT)  
FEATURES Location/Qualifiers  
Source 1..15  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Primer"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 ACCGCGCGCGG 399  
Db 4 ACCGCGCGCGG 14

RESULT 252  
LOCUS AX633447 15 bp RNA  
DEFINITION Sequence 586 from Patent EP1260586.  
ACCESSION AX633447  
VERSION AX633447.1 GI:28469061  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

REFERENCE 1  
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Dizenzo, A., Karpelsky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 586 27-NOV-2002;  
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)  
Source 1..15  
/organism="unidentified"  
/mol\_type="unassigned RNA"  
/db\_xref="taxon:32644"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGGAG 254  
Db 4 ACCCTCTGGAG 14

RESULT 253  
LOCUS AX633488 15 bp RNA  
DEFINITION Sequence 627 from Patent EP1260586.  
ACCESSION AX633488  
VERSION AX633488.1 GI:28469102  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Dizenzo, A., Karpelsky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.  
TITLE Method and reagent for inhibiting the expression of disease related genes  
JOURNAL Patent: EP 1260586-A 627 27-NOV-2002;  
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)  
Source 1..15  
/organism="unidentified"  
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/db\_xref="taxon:32644"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGGAG 254  
Db 4 ACCCTCTGGAG 14

RESULT 254  
LOCUS AX633547 15 bp RNA  
DEFINITION Sequence 686 from Patent EP1260586.  
ACCESSION AX633547  
VERSION AX633547.1 GI:28469161  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified

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REFERENCE
AUTHORS
1
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 686 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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Query Match
1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
244 ACCTCCTGGAG 254
|||||
4 ACCTCCTGGAG 14
Db

RESULT 255
AX635687/c
LOCUS
AX635687 15 bp RNA linear PAT 24-FEB-2003
DEFINITION
Sequence 2826 from Patent EP1260586.
ACCESSION
AX635687
VERSION
AX635687.1 GI:28471301
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 2826 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
location/Qualifiers
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
441 CTGGAACTT 451
|||||
12 CTGGAACTT 2
Db

RESULT 256
AX635689/c
LOCUS
AX635689 15 bp RNA linear PAT 21-FEB-2003
DEFINITION
Sequence 2828 from Patent EP1260586.
ACCESSION
AX635689
VERSION
AX635689.1 GI:28471303
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1

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AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 2828 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
ORIGIN
Query Match
1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
441 CTGGAACTT 451
|||||
11 CTGGAACTT 1
Db

RESULT 257
AX635691/c
LOCUS
AX635691 15 bp RNA linear PAT 21-FEB-2003
DEFINITION
Sequence 2830 from Patent EP1260586.
ACCESSION
AX635691
VERSION
AX635691.1 GI:28471305
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE
Method and reagent for inhibiting the expression of disease related
genes
JOURNAL
Patent: EP 1260586-A 2830 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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/mol_type="unassigned RNA"
/db_xref="taxon:32644"
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Query Match
1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY
441 CTGGAACTT 451
|||||
11 CTGGAACTT 1
Db

RESULT 258
BD206999/c
LOCUS
BD206999 15 bp RNA linear PAT 17-UTL-2003
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION
BD206999
VERSION
BD206999.1 GI:33016769
KEYWORDS
unidentified
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 15)

```

AUTHORS Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.  
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
 JOURNAL Patent: JP 2002512791-A 589 08-MAY-2002;  
 RIBOZYME PHARMACEUTICALS INC  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002512791-A/589  
 PD 08-MAY-2002  
 PF 26-APR-1999 JP 2000545991  
 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR  
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI  
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PAVCO, PAVCO, PI  
 DENNIS MACEJAK  
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09, A61K37/66,  
 PC C12N15/00  
 CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
 FT source Location/Qualifiers  
 1.15  
 /organism="Hepatitis virus (hepatitis C virus)"  
 /db\_xref="taxon:32644"

FEATURES  
 source Location/Qualifiers  
 1.15  
 /organism="unidentified"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:32644"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGACCCC 369  
 |||||  
 13 AGGCTGACCCC 3

Db

RESULT 259  
 BD208353 15 bp RNA linear PAT 17-JUN-2003  
 LOCUS Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
 DEFINITION BD208353  
 ACCESSION BD208353.1 GI:33018123  
 VERSION JP 2002512791-A/1943.  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.

REFERENCE 1 (bases 1 to 15)  
 Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.  
 TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection  
 JOURNAL Patent: JP 2002512791-A 1943 08-MAY-2002;  
 RIBOZYME PHARMACEUTICALS INC  
 OS Hepatitis virus (hepatitis C virus)  
 PN JP 2002512791-A/1943  
 PD 08-MAY-2002  
 PF 26-APR-1999 JP 2000545991  
 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR  
 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI  
 LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PAVCO, PAVCO, PI  
 DENNIS MACEJAK  
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09, A61K37/66,  
 PC C12N15/00  
 CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.  
 FT source Location/Qualifiers  
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 /mol\_type="genomic RNA"  
 /db\_xref="taxon:32644"

FT source 1.15  
 /organism="Hepatitis virus (hepatitis C virus)"  
 /db\_xref="taxon:32644"

FEATURES  
 source Location/Qualifiers  
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 /organism="unidentified"  
 /mol\_type="genomic RNA"  
 /db\_xref="taxon:32644"

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 Query Match 1.8%; Score 11; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 CTGGGCTAAG 67  
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 1 CTGGGCTAAG 11

Db

RESULT 260  
 A66853 16 bp DNA linear PAT 29-MAR-1999  
 LOCUS Sequence 20 from Patent WO9740193.  
 DEFINITION A66853  
 ACCESSION A66853.1 GI:4538224  
 VERSION A66853.1  
 KEYWORDS unidentified  
 SOURCE unidentified  
 ORGANISM unidentified  
 unclassified.

REFERENCE 1 (bases 1 to 16)  
 Stuyver, L., Rossau, R. and Maertens, G.  
 TITLE METHOD FOR TYPING AND DETECTING HBV  
 JOURNAL Patent: WO 9740193-A 20 30-OCT-1997;  
 INNOGENETICS NV (BE)  
 Location/Qualifiers  
 1.16  
 /organism="unidentified"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32644"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 ACTGCTGGAT 447  
 |||||  
 13 ACTGCTGGAT 3

Db

RESULT 261  
 AR089188 16 bp DNA linear PAT 07-SEP-2000  
 LOCUS Sequence 4 from patent US 5994056.  
 DEFINITION AR089188  
 ACCESSION AR089188  
 VERSION AR089188.1 GI:10015945  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 unclassified.

REFERENCE 1 (bases 1 to 16)  
 Higuchi, R.G.  
 TITLE Homogeneous methods for nucleic acid amplification and detection  
 JOURNAL Patent: US 5994056-A 4 30-NOV-1999;  
 Location/Qualifiers  
 1.16  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

ORIGIN  
 Query Match 1.8%; Score 11; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229  
Db 11 CCGCTGCTACC 1

RESULT 262  
ARI23643/c 16 bp DNA linear PAT 16-MAY-2001  
LOCUS  
DEFINITION Sequence 4 from patent US 6171785.  
ACCESSION ARI23643  
VERSION ARI23643.1 GI:14109004  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Higuchi,R.G.  
TITLE Methods and devices for homogeneous nucleic acid amplification and detector

JOURNAL  
FEATURES  
Source  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229  
Db 11 CCGCTGCTACC 1

RESULT 263  
I14457 16 bp DNA linear PAT 26-SEP-1995  
LOCUS  
DEFINITION Sequence 31 from patent US 5449768.  
ACCESSION I14457  
VERSION I14457.1 GI:996940  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Chakraborty,P.R., Dashkevicz,M., Eldbrecht,A., Feigheimer,S.D.,  
Liberator,P.A. and Profous-Juchelka,H.  
TITLE Eimeria praecox 16S rDNA probes  
JOURNAL Patent: US 5449768-A 31-12-SEP-1995;  
FEATURES  
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Location/Qualifiers  
1. .16  
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ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365  
Db 3 CGCAGGCTGA 13

RESULT 264  
I27300 16 bp DNA linear PAT 06-FEB-1997  
LOCUS  
DEFINITION Sequence 31 from patent US 5563256.  
ACCESSION I27300  
VERSION I27300.1 GI:1818076  
KEYWORDS

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Chakraborty,P.R., Dashkevicz,M., Eldbrecht,A., Feigheimer,S.D.,  
Liberator,P.A. and Profous-Juchelka,H.  
TITLE Eimeria tenella 16S rDNA probes  
JOURNAL Patent: US 5563256-A 31-08-OCT-1996;  
FEATURES  
Source  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365  
Db 3 CGCAGGCTGA 13

RESULT 265  
I27973 16 bp DNA linear PAT 06-FEB-1997  
LOCUS  
DEFINITION Sequence 145 from patent US 5567809.  
ACCESSION I27973  
VERSION I27973.1 GI:1818749  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.  
TITLE Methods and reagents for HLA DRbeta DNA typing  
JOURNAL Patent: US 5567809-A 145 22-OCT-1996;  
FEATURES  
Source  
Location/Qualifiers  
1. .16  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGAGC 255  
Db 1 CCTCCTGAGC 11

RESULT 266  
I27980 16 bp DNA linear PAT 06-FEB-1997  
LOCUS  
DEFINITION Sequence 152 from patent US 5567809.  
ACCESSION I27980  
VERSION I27980.1 GI:1818756  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.  
TITLE Methods and reagents for HLA DRbeta DNA typing  
JOURNAL Patent: US 5567809-A 152 22-OCT-1996;  
FEATURES  
Source  
Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255  
Db 16 CCTCCTGGAGC 6

## RESULT 267

LOCUS 127982 16 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 154 from patent US 5567809.

ACCESSION 127982 GI:1818758

VERSION 127982.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS Apple, R.J., Erlich, H.A., Griffith, R.L. and Scharf, S.J.

TITLE Methods and reagents for HLA DRbeta DNA typing

JOURNAL Patent: US 5567809-A 154 22-OCT-1996;

FEATURES

source 1.16  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255  
Db 1 CCTCCTGGAGC 11

## RESULT 268

LOCUS BD093179 16 bp DNA linear PAT 27-AUG-2002

DEFINITION A gene cooding a cyclic lopopeptide acylase and an expression thereof.

ACCESSION BD093179

VERSION BD093179.1 GI:22638767

KEYWORDS WO 0102585-A/42.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 16)

AUTHORS Shibata, T., Noguchi, Y. and Ymashita, M.

TITLE A gene cooding a cyclic lopopeptide acylase and an expression

JOURNAL Patent: WO 0102585-A 42 11-JAN-2001;

FEATURES FUJISAWA PHARMACEUTICAL CO LTD, TAKASHI SHIBATA, YUJI NOGUCHI, MICHIO YMAISHITA

COMMENT OS Artificial Sequence

PN WO 0102585-A/42

PD 11-JAN-2001

PF 28-JUN-2000 WO 2000JP004285

PR 02-JUL-1999 JP 99P 189644

PI TAKASHI SHIBATA, YUJI NOGUCHI, MICHIO YMAISHITA

PC C12N15/55, C12N1/21, C12N9/14

CC Oligonucleotide designed to act as sequencing primer. FH Key

FEATURES Location/Qualifiers

source 1.16  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GAGACCTACT 86

Db 4 GAGACCTACT 14

## RESULT 269

LOCUS A42338 17 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 10 from Patent WO9502057.

ACCESSION A42338 GI:2297815

VERSION A42338.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 17)

AUTHORS Gusterson, B.A., Crompton, M.R., Mitchell, P.J., Barker, K.T.,

Kamat, T., Page, M.J. and Spence, P.

TITLE PROTEIN TYROSINE KINASE AND LIGANDS THEREOF

JOURNAL Patent: WO 9502057-A 10 19-JAN-1995;

COMMENT CANCER RES INST (GB)

Other publication AU 7080994 950206.

FEATURES

source 1.17  
/organism="unidentified"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32644"

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 GCCACGTGGA 174  
Db 4 GCCACGTGGA 14

## RESULT 270

LOCUS AR039557 17 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 405 from patent US 5807743.

ACCESSION AR039557

VERSION AR039557.1 GI:5958920

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb, D.T. and McSwigen, J.A.

TITLE Interleukin-2 receptor gamma-chain ribozymes

JOURNAL Patent: US 5807743-A 405 15-SEP-1998;

FEATURES Location/Qualifiers

source 1.17  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGCCCC 547  
Db 6 CCTTTGCCCC 16

## RESULT 271

LOCUS AR039559 17 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 407 from patent US 5807743.

ACCESSION AR039559

VERSION AR039559.1 GI:5958922  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.  
 TITLE Interleukin-2 receptor gamma-chain ribozymes  
 JOURNAL Patent: US 5807743-A 407 15-SEP-1998;  
 FEATURES Location/Qualifiers  
 source 1..17

ORIGIN /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGCCCC 547  
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 Db 5 CCTTTGCCCC 15

RESULT 272  
 LOCUS AR039561 17 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 409 from patent US 5807743.  
 ACCESSION AR039561  
 VERSION AR039561.1 GI:5958924  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.  
 TITLE Interleukin-2 receptor gamma-chain ribozymes  
 JOURNAL Patent: US 5807743-A 409 15-SEP-1998;  
 FEATURES Location/Qualifiers  
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ORIGIN /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGCCCC 547  
 |||||  
 Db 4 CCTTTGCCCC 14

RESULT 273  
 LOCUS AR057431 17 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 1635 from patent US 5837542.  
 ACCESSION AR057431  
 VERSION AR057431.1 GI:5983008  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 1635 17-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..17

ORIGIN /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
 |||||  
 Db 5 TGCTCTTCCTC 15

RESULT 274  
 LOCUS AR057487 17 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 1691 from patent US 5837542.  
 ACCESSION AR057487  
 VERSION AR057487.1 GI:5983064  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 1691 17-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..17

ORIGIN /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
 |||||  
 Db 5 TGCTCTTCCTC 15

RESULT 275  
 LOCUS AR057566 17 bp DNA PAT 29-SEP-1999  
 DEFINITION Sequence 1770 from patent US 5837542.  
 ACCESSION AR057566  
 VERSION AR057566.1 GI:5983143  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
 JOURNAL Patent: US 5837542-A 1770 17-NOV-1998;  
 FEATURES Location/Qualifiers  
 source 1..17

ORIGIN /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186  
 |||||  
 Db 3 TGCTCTTCCTC 13

RESULT 276  
 LOCUS AR057626 17 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 1830 from patent US 5837542.  
ACCESSION AR057626  
VERSION AR057626.1 GI:5983203  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1830 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 ACCTCCTGGAG 254  
|||||  
5 ACCTCCTGGAG 15  
Db  
RESULT 277  
AR057632 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1836 from patent US 5837542.  
DEFINITION AR057632  
ACCESSION AR057632  
VERSION AR057632.1 GI:5983209  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1836 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 ACCTCCTGGAG 254  
|||||  
5 ACCTCCTGGAG 15  
Db  
RESULT 278  
AR057687 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1891 from patent US 5837542.  
DEFINITION AR057687  
ACCESSION AR057687  
VERSION AR057687.1 GI:5983264  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1891 17-NOV-1998;  
FEATURES Location/Qualifiers

source 1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
|||||  
5 TGCTCTTCCTC 15  
Db  
RESULT 279  
AR057690 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1894 from patent US 5837542.  
DEFINITION AR057690  
ACCESSION AR057690  
VERSION AR057690.1 GI:5983267  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1894 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
|||||  
2 TGCTCTTCCTC 12  
Db  
RESULT 280  
AR057764 17 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 1968 from patent US 5837542.  
DEFINITION AR057764  
ACCESSION AR057764  
VERSION AR057764.1 GI:5983341  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1968 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 244 ACCTCCTGGAG 254  
|||||  
5 ACCTCCTGGAG 15  
Db

RESULT 261  
LOCUS AR057777 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1981 from patent US 5837542.  
ACCESSION AR057777  
VERSION AR057777.1 GI:5983354  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1981 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
Db 5 TGCTCTTCCTC 15

RESULT 282  
LOCUS AR057780 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1984 from patent US 5837542.  
ACCESSION AR057780  
VERSION AR057780.1 GI:5983357  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1984 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
Db 5 TGCTCTTCCTC 15

RESULT 283  
LOCUS AR057782 17 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 1986 from patent US 5837542.  
ACCESSION AR057782  
VERSION AR057782.1 GI:5983359  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

Draper,K.G.  
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes  
JOURNAL Patent: US 5837542-A 1986 17-NOV-1998;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
Db 5 TGCTCTTCCTC 15

RESULT 284  
LOCUS AR115189 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1635 from patent US 6132367.  
ACCESSION AR115189  
VERSION AR115189.1 GI:14095511  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132367-A 1635 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
Db 5 TGCTCTTCCTC 15

RESULT 285  
LOCUS AR115245 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1691 from patent US 6132367.  
ACCESSION AR115245  
VERSION AR115245.1 GI:14095567  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132367-A 1691 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 176 TGCTCTTCCTC 186  
Db 5 TGCTCTTCCTC 15

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186  
|||||  
5 TGCTCTTCTC 15

Db 5 TGCTCTTCTC 15

RESULT 286  
AR115324  
LOCUS AR115324 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1770 from patent US 6132967.  
ACCESSION AR115324  
VERSION AR115324.1 GI:14095646  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1770 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186  
|||||  
3 TGCTCTTCTC 13

Db 3 TGCTCTTCTC 13

RESULT 287  
AR115384  
LOCUS AR115384 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1830 from patent US 6132967.  
ACCESSION AR115384  
VERSION AR115384.1 GI:14095706  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1830 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
|||||  
5 ACCTCCTGGAG 15

Db 5 ACCTCCTGGAG 15

RESULT 288  
AR115390  
LOCUS AR115390 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1836 from patent US 6132967.

ACCESSION AR115390  
VERSION AR115390.1 GI:14095712  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1836 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254  
|||||  
5 ACCTCCTGGAG 15

Db 5 ACCTCCTGGAG 15

RESULT 289  
AR115445  
LOCUS AR115445 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1891 from patent US 6132967.  
ACCESSION AR115445  
VERSION AR115445.1 GI:14095767  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
JOURNAL Patent: US 6132967-A 1891 17-OCT-2000;  
FEATURES Location/Qualifiers  
1..17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186  
|||||  
5 TGCTCTTCTC 15

Db 5 TGCTCTTCTC 15

RESULT 290  
AR115448  
LOCUS AR115448 17 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1894 from patent US 6132967.  
ACCESSION AR115448  
VERSION AR115448.1 GI:14095770  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 17)  
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTCTCCTC 186  
 |||||  
 Db 2 TGCTCTCTCCTC 12

## RESULT 291

AR115522 17 bp DNA linear PAT 16-MAY-2001  
 LOCUS  
 DEFINITION Sequence 1968 from patent US 6132967.  
 ACCESSION AR115522  
 VERSION AR115522.1 GI:14095844  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
 JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTCGAG 254  
 |||||  
 Db 5 ACCTCCTCGAG 15

## RESULT 292

AR115535 17 bp DNA linear PAT 16-MAY-2001  
 LOCUS  
 DEFINITION Sequence 1981 from patent US 6132967.  
 ACCESSION AR115535  
 VERSION AR115535.1 GI:14095857  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
 JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTCTCCTC 186  
 |||||  
 Db 5 TGCTCTCTCCTC 15

## RESULT 293

AR115538 17 bp DNA linear PAT 16-MAY-2001  
 LOCUS  
 DEFINITION Sequence 1984 from patent US 6132967.  
 ACCESSION AR115538  
 VERSION AR115538.1 GI:14095860  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
 JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTCTCCTC 186  
 |||||  
 Db 2 TGCTCTCTCCTC 12

## RESULT 294

AR115540 17 bp DNA linear PAT 16-MAY-2001  
 LOCUS  
 DEFINITION Sequence 1986 from patent US 6132967.  
 ACCESSION AR115540  
 VERSION AR115540.1 GI:14095862  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.  
 TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)  
 JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;  
 FEATURES Location/Qualifiers  
 source 1..17  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTCTCCTC 186  
 |||||  
 Db 5 TGCTCTCTCCTC 15

## RESULT 295

AR142556 17 bp DNA linear PAT 08-AUG-2001  
 LOCUS  
 DEFINITION Sequence 15 from patent US 6203801.  
 ACCESSION AR142556  
 VERSION AR142556.1 GI:15103842

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
JOURNAL Coccidioides polysaccharide and vaccines  
PATENT: US 6203801-A 15 20-MAR-2001;  
FEATURES Location/Qualifiers  
source 1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 TTGGGACTTTG 596  
|||||  
6 TTGGGACTTTG 16

Db 6 TTGGGACTTTG 16

RESULT 296  
LOCUS AR142558 17 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 17 from patent US 6203801.  
ACCESSION AR142558  
VERSION AR142558.1 GI:15103844  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
JOURNAL Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.  
PATENT: US 6203801-A 17 20-MAR-2001;  
FEATURES Location/Qualifiers  
source 1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 TTGGGACTTTG 596  
|||||  
6 TTGGGACTTTG 16

Db 6 TTGGGACTTTG 16

RESULT 297  
LOCUS AR142560 17 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 19 from patent US 6203801.  
ACCESSION AR142560  
VERSION AR142560.1 GI:15103846  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
JOURNAL Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.  
PATENT: US 6203801-A 19 20-MAR-2001;  
FEATURES Location/Qualifiers  
source 1. 17  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 TTGGGACTTTG 596  
|||||  
6 TTGGGACTTTG 16

Db 6 TTGGGACTTTG 16

Best Local Similarity 100.0%; Pred.No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 TTGGGACTTTG 596  
|||||  
6 TTGGGACTTTG 16

Db 6 TTGGGACTTTG 16

RESULT 298  
LOCUS AR142562 17 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 21 from patent US 6203801.  
ACCESSION AR142562  
VERSION AR142562.1 GI:15103848  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
JOURNAL Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.  
PATENT: US 6203801-A 21 20-MAR-2001;  
FEATURES Location/Qualifiers  
source 1. 17  
/organism="unknown"  
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ORIGIN  
Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred.No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 586 TTGGGACTTTG 596  
|||||  
6 TTGGGACTTTG 16

Db 6 TTGGGACTTTG 16

RESULT 299  
LOCUS BD254479 17 bp DNA linear PAT 17-JUL-2003  
DEFINITION Regulation of repressor genes using nucleic acid molecules.  
ACCESSION BD254479  
VERSION BD254479.1 GI:33064249  
KEYWORDS JP 2002541795-A/2272.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
AUTHORS 1 (bases 1 to 17)  
TITLE Unclassified.  
JOURNAL Blatt,L., Zwick,M., Pavco,P. and McSwiggen,J.  
PATENT: JP 2002541795-A 2272 10-DEC-2002;  
COMMENT RIBOZYME PHARMACEUTICALS INC  
OS Eukaryote  
PN JP 2002541795-A/2272  
PD 10-DEC-2002  
PF 11-APR-2000 JP 2000611654  
PI 12-APR-1999 US 60/128390  
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC  
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC  
C12P21/02,  
PC C12P21/02,A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC  
C12R1:91)  
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
PC A61K37/02,  
PC (C12N5/00,C12R1:91)  
CC Regulation of repressor genes using nucleic acid molecules FH  
Key Location/Qualifiers  
FT source 1. 17  
Location/Qualifiers  
1. 17  
/organism="Eukaryote",  
/organism="unidentified"

ORIGIN

/mol\_type="genomic DNA"  
/db\_xref="taxon:32644"

Query Match 1.8%; Score 11; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.3e+06;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 CTCTCCAGACA 524  
|||||  
Db 7 CTCTCCAGACA 17

RESULT 300

BD254480 17 bp DNA linear PAT 17-JUL-2003  
DEFINITION Regulation of repressor genes using nucleic acid molecules.

LOCUS BD254480

ACCESSION BD254480

VERSION BD254480.1 GI:33064250

KEYWORDS JP 2002541795-A/2273.

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 17)

Autors, L., Zwick, M., Pavco, P. and McSwiggen, J.

Regulation of repressor genes using nucleic acid molecules

Patent: JP 2002541795-A 2273 10-DEC-2002;

RIBOZYME PHARMACEUTICALS INC

OS Eukaryote

PN JP 2002541795-A/2273

PD 10-DEC-2002 JP 200611654

PR 11-APR-2000 JP 200611654

PI 12-APR-1999 US 60/129390

PI LAWRENCE BLATT, MICHAEL, ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC

C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC

C12P21/02, PC

C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC

C12R1:91),

PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,

PC A61K37/02,

PC (C12N5/00, C12R1:91)

CC Regulation of repressor genes using nucleic acid molecules FH

Key Location/Qualifiers

FT source 1..17

Location/Qualifiers

1..17

/organism="unidentified"

/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 CTCTCCAGACA 524

|||||

Db 5 CTCTCCAGACA 15

Search completed: March 4, 2004, 22:53:41  
Job time : 2790 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 5, 2004, 00:22:13 ; Search time 2507 Seconds  
(without alignments)  
2358.481 Million cell updates/sec

## SUMMARIES

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: US-09-966-880A-8  
Perfect score: 198  
Sequence: 1 MDSLLMRKFLYQKKNRW.....ILLFLYVDDLRDAFRTGL 198

Scoring table: OLIGO  
Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 7974

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2.1/USPTO/US09966880/runat\_04032004\_08153\_22395/app\_query.fasta\_1.391  
-DB=EST -QFMT=fastap -SUFFIX=Oligo.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=Oligo -TRANS=human40.cdi -LIST=45  
-LOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=300 -MODE=LOCAL -OUTFMT=ptc  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20  
-USER=US09966880 @CGN 1.1 3437 @runat\_04032004\_08153\_22395 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6  
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estlin.\*  
4: em\_estmu.\*  
5: em\_estrov.\*  
6: em\_estrpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_hiv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_yrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rtd.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*

Result No.	Score	Query Match	Length	DB ID	Description
1	4	2.0	14	12	BM397622
2	4	2.0	14	12	BM398220
3	4	2.0	14	12	BM398220
4	4	2.0	14	12	BM398220
5	4	2.0	14	12	BM398220
6	4	2.0	14	12	BM398220
7	4	2.0	14	12	BM398220
8	4	2.0	14	12	BM398220
9	4	2.0	14	12	BM398220
10	4	2.0	14	12	BM398220
11	4	2.0	14	12	BM398220
12	4	2.0	14	12	BM398220
13	4	2.0	14	12	BM398220
14	4	2.0	14	12	BM398220
15	4	2.0	14	12	BM398220
16	4	2.0	14	12	BM398220
17	4	2.0	14	12	BM398220
18	4	2.0	14	12	BM398220
19	4	2.0	14	12	BM398220
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24	4	2.0	14	12	BM398220
25	4	2.0	14	12	BM398220
26	4	2.0	14	12	BM398220
27	4	2.0	14	12	BM398220
28	4	2.0	14	12	BM398220
29	4	2.0	14	12	BM398220
30	4	2.0	14	12	BM398220
31	4	2.0	14	12	BM398220
32	4	2.0	14	12	BM398220
33	4	2.0	14	12	BM398220
34	4	2.0	14	12	BM398220
35	4	2.0	14	12	BM398220
36	4	2.0	14	12	BM398220
37	4	2.0	14	12	BM398220
38	4	2.0	14	12	BM398220
39	4	2.0	14	12	BM398220
40	4	2.0	14	12	BM398220
41	4	2.0	14	12	BM398220
42	4	2.0	14	12	BM398220
43	4	2.0	14	12	BM398220
44	4	2.0	14	12	BM398220
45	4	2.0	14	12	BM398220

## ALIGNMENTS

RESULT 1  
BM397622  
LOCUS  
DEFINITION  
5009-0-35-C02.t.2 Chiloat/Turkewitz CDNA (large fraction)  
ACCESSION  
BM397622  
VERSION  
BM397622.1 GI:18197675  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 14)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,J.  
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells  
JOURNAL Unpublished (2002)  
COMMENT Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3

FEATURES  
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Location/Qualifiers  
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/note="Vector: Bluescript2 SK+, Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.23e+05 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM397622 (1-14)

Cy 120 LysalagluPro 123

Db 2 AAAGCTGAGCCA 13

RESULT 2  
BM398220/c 14 bp mRNA linear EST 17-JAN-2002  
LOCUS 5009-0-42-D11.c.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM398220  
VERSION BM398220.1 GI:18198273  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 14)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,J.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3  
Location/Qualifiers

FEATURES  
source  
1. .14  
Location/Qualifiers  
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/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+, Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.23e+05 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398220 (1-14)

Cy 167 GluAenSerVal 170  
Db 14 GAGAAATAGTGTA 3

RESULT 3  
CA850755/c 14 bp mRNA linear EST 01-AUG-2003  
LOCUS D06B10.B10.04.ab1 cDNA Peking library 2, 4 day SCN3 glycine max  
DEFINITION cDNA clone D06B10 5', mRNA sequence.  
ACCESSION CA850755  
VERSION CA850755.1 GI:33387548  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;  
glycine.  
1 (bases 1 to 14)  
Alkharout,N.W., Khan,R. and Matthews,B.F.  
Analysis of expressed sequence tags from roots of resistant soybean  
infected by the soybean cyst nematode  
Unpublished (2002)  
Contact: Alkharout, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharout@da.ars.usda.gov.  
Location/Qualifiers

FEATURES  
source  
1. .14  
Location/Qualifiers  
/organism="Glycine max"  
/mol\_type="RNA"  
/cultivar="Peking"  
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/tissue\_type="Roots"  
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## ORIGIN

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Pred. No.: 3.23e+05 Length: 14  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA850755 (1-14)

Cy 41 SerPheSerLeu 44  
Db 12 AGTTTAGTCCT 1

RESULT 4  
BQ584986

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LOCUS      BQ584986                15 bp    mRNA    linear    EST 06-BEC-2002
DEFINITION E011826-024-002-K24-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
ACCESSION  BQ584986
VERSION    BQ584986.1   GI:26114563
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 15)
            Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lennach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE    12472698
COMMENT    Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mpiz-koeln.mpg.de
            Insert Length: 15    Std Error: 0.00
            Plate: 2    row: K    column: 24
            Seq primer: SP6; CATACGATTAGTGACACACTAG.
            Location/Qualifiers
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                line)"
                /db_xref="GABI:181716"
                /db_xref="taxon:161934"
                /clone="024-002-K24"
                /tissue_type="inflorescence"
                /lab_host="EMDHI08"
                /clone_1ib="MP1Z-ADIS-024-inflorescence"
                /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                orientation:
                SP6-Sali-CCACGCGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                Project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Alignment Scores:
Pred. No.:      3.47e+05      Length:      15
Score:          4.00          Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.02%        Indels:      0
DB:             13           Gaps:       0

US-09-966-880A-8 (1-198) x BQ584986 (1-15)
QY          177  AAAAAAGTAACTT 180
DB          2  AAAAAAGTAACTT 13

RESULT 5
LOCUS     A1075064                16 bp    mRNA    linear    EST 27-ANG-1998
DEFINITION OAG1911.X1 NCI CGAP Br-2 Homo sapiens cDNA clone IMAGE:1632356 3'
            similar to TR:Q24348 Q24348 FIBRILARIN ;, mRNA sequence.
ACCESSION A1075064

```

```

VERSION    A1075064.1   GI:3399844
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 16)
            NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LINL at:
            www.bio.lnl.gov/bdrp/image/image.html
            Insert Length: 712    Std Error: 0.00
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            High quality sequence stop: 1.
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                /clone="IMAGE:1632356"
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                /clone_1ib="NCI CGAP Br-2"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; 1st strand cDNA was prepared from pooled bulk
                breast tumor tissue, and was then primed with a Not I -
                oligo(dT) primer. Double-stranded cDNA was ligated to Eco
                RI adaptors (Pharmacia), digested with Not I and cloned
                into the Not I and Eco RI sites of the modified pT7T3
                vector. This library is the normalized version of
                NCI CGAP Br1.1. Library was constructed by Bento Soares
                and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.:      3.72e+05      Length:      16
Score:          4.00          Matches:      4
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    2.02%        Indels:      0
DB:             9           Gaps:       0

US-09-966-880A-8 (1-198) x A1075064 (1-16)
QY          180  LeuAUPProLeu 183
DB          1  CTCCTCCCCCTC 12

RESULT 6
LOCUS     A1188895                16 bp    mRNA    linear    EST 28-OCT-1998
DEFINITION Gd5b06.x1 Soares fetal heart NBDH19W Homo sapiens cDNA clone
            IMAGE:1731539 3' similar to SM:SN22 HUMAN P51531 POSSIBLE GLOBAL
            TRANSCRIPTION ACTIVATOR SNF2L2 ;, mRNA sequence.
ACCESSION A1188895
VERSION    A1188895.1   GI:3740104
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 16)

```

**AUTHORS** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Tumor Gene Index  
**COMMENT** Unpublished (1997)  
 Contact: Robert Straubeberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 This clone is available royalty-free through LINTL; contact the  
 IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 Trace considered overall poor quality  
 Insert length: 543 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers

# FEATURES

source

1.16  
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 /dev\_stage="19 weeks"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_fetal\_heart\_NDHL9W"  
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a  
 modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACCATCTGAGTGGAGCGCCGATCTTTTCTTTTCTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT73 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by  
 M.Fatima Bonaldo. This library was constructed from the  
 same fetus as the fetal lung library, Soares fetal lung  
 NDHL9W."

# ORIGIN

## Alignment Scores:

Pred. No.: 3.72e+05 Length: 16  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A118895 (1-16)

QY 94 ValAlaapPhe 97  
 Db 5 GTTGCACACTTT 16

**RESULT 7** BG926060 16 bp mRNA linear EST 06-NOV-2001  
**LOCUS** BG926060  
**DEFINITION** HNC23-1-Fl.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 sequence.  
**ACCESSION** BG926060  
**VERSION** BG926060.1 GI:14320583  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
**AUTHORS** 1 (bases 1 to 16)  
 Sathie,G., Mol,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
**JOURNAL** Osteoarthritis Cartil. 9 (7), 641-653 (2001)  
**MEDLINE** 21482651  
**PUBMED** 11597177  
**COMMENT** Contact: Sanjay Kumar

UN2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: [sanjay.kumar@lgsk.com](mailto:sanjay.kumar@lgsk.com)  
 Seq primer: T7.  
 Location/Qualifiers  
 1.16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E. coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"

# ORIGIN

**Alignment Scores:**  
 Pred. No.: 3.72e+05 Length: 16  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG926060 (1-16)

QY 59 LeuLeuPheLeu 62  
 Db 2 CTCTCTCTCTT 13

**RESULT 8** AA885697 19 bp mRNA linear EST 09-JUN-1998  
**LOCUS** AA885697  
**DEFINITION** OJ34f01.s1 NCI-CGAP LUS Homo sapiens cDNA clone IMAGE:1500217 3'  
 similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPPL. [1] ; mRNA  
 sequence.  
**ACCESSION** AA885697  
**VERSION** AA885697.1 GI:3000805  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
**REFERENCE** NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
**AUTHORS** 1 (bases 1 to 19)  
**TITLE** National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
**JOURNAL** Unpublished (1997)  
**COMMENT** Contact: Robert Straubeberg, Ph.D.  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINTL at:  
[www-bio.llnl.gov/bdip/image/image.html](http://www-bio.llnl.gov/bdip/image/image.html)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINTL at:  
[www-bio.llnl.gov/bdip/image/image.html](http://www-bio.llnl.gov/bdip/image/image.html)  
 Insert length: 691 Std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 1.

## FEATURES

source

Location/Qualifiers  
1. .19

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1500217"  
/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Lus"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AA885697 (1-19)

QY 127 ArgArgLeuHis 130

Db 8 AGCGCGTTCAT 19

## RESULT 9

CNS08V6Z

LOCUS

19 bp mRNA linear HTC 07-JAN-2003

Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone

FK0AAA4CD05 of strain 6-9 of Anopheles gambiae (African malaria mosquito).

ACCESSION BX029847

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="6-9"  
/db\_xref="taxon:7165"  
/clone="FK0AAA4CD05"  
/plasmid="pME185-FL"  
/note="end : 3-PRIME"

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	11	Gaps:	0

US-09-966-880A-8 (1-198) x CNS08V6Z (1-19)

QY 59 LeuLeuPheLeu 62

Db 1 CTCCTCTTCCT 12

## RESULT 10

CF305339

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF305339 19 bp mRNA linear EST 15-AUG-2003  
CLD1--01-H03.b1 Rice cold treated leaf plasmid cDNA library (CLD1)  
Oryza sativa cDNA clone CLD1--01-H03, mRNA sequence.  
CF305339  
CF305339.1 GI:33677100  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Naim, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Naim, B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnaim@gbio.com, bhnaim@bio.myongji.ac.kr.  
Location/Qualifiers

## FEATURES

source

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="CLD1--01-H03"  
/issue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF305339 (1-19)

QY 36 ArgArgSerAla 39

Db 6 CGGACTCTGCT 17

## RESULT 11

CF316655

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

CF316655 19 bp mRNA linear EST 15-AUG-2003  
HD--06-A14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--06-A14, mRNA sequence.  
CF316655  
CF316655.1 GI:33688416  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharciodeae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Biocscience and Bioinformatics, Yonsei University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
location/Qualifiers  
1..19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--06-A14"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2M6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDACL-overexpressing transgenic rice plasmid  
CDNA library (HD)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

Alignment Scores:  
Pred. No.: 4.48e+05 Length: 19  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF31655 (1-19)

QY 59 Leuleupheleu 62  
DB 1 CTTTATTCCTG 12

RESULT 12  
CF337608/c 19 bp mRNA linear EST 18-AUG-2003  
LOCUS  
DEFINITION  
JMT--08-C02.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--08-C02, mRNA sequence.  
ACCESSION  
CF337608  
VERSION  
CF337608.1 GI:33823602  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharciodeae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Biocscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

location/Qualifiers

## source

1..19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--08-C02"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
CDNA library (JMT)"  
/note="Vector: PCR4-TOPO, Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

## ORIGIN

Alignment Scores:  
Pred. No.: 4.48e+05 Length: 19  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF337608 (1-19)

QY 59 Leuleupheleu 62  
DB 14 CTCCTCTTCTT 3

RESULT 13  
AZ307864/c 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION  
1M0010F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0010F16 F, genomic survey sequence.  
ACCESSION  
AZ307864  
VERSION  
AZ307864.1 GI:10347281  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0010 row: F column: 16  
Seq primer: CGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0010F16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone.lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ307864 (1-19)

Qy 125 GYLeuArgArg 128  
 |||||  
 18 GGCTTACGCCGG 7

RESULT 14 19 bp DNA linear GSS 29-SEP-2000  
 AZ309643  
 LOCUS 1M0016E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0016E23 F, genomic survey sequence.  
 AZ309643  
 ACCESSION AZ309643.1 GI:10350661  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE  
 ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tilgney,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0016 row: B column: 23  
 Seg primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.  
 location/Qualifiers  
 1..19  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ309643 (1-19)

Qy 167 GLUanSerVal 170  
 |||||  
 Db 15 GAGAACTCTGTG 4

RESULT 15 19 bp DNA linear GSS 02-OCT-2000  
 AZ361152  
 LOCUS 1M0104A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0104A16 R, genomic survey sequence.  
 AZ361152  
 ACCESSION AZ361152.1 GI:10474852  
 VERSION GSS.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE  
 ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 19)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tilgney,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
 University of Utah  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0104 row: A column: 16  
 Seg primer: CACACGAAACGCTATGAC  
 Class: plasmid ends

FEATURES High quality sequence strip: 19.  
Location/Qualifiers

1.19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U081M010416"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid U081M library"  
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ394192 (1-19)

QY 85 SerProCysTyr 88  
|||||  
DB 4 ACCCATGCTAC 15

## RESULT 16

AZ394192 19 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0157609R Mouse 10kb plasmid U081M library Mus musculus genomic  
DEFINITION clone U081M0157609 R, genomic survey sequence.

ACCESSION AZ394192  
VERSION AZ394192.1 GI:10509264  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0157 row: G column: 09  
Seq primer: CACACGAGAAACGCTATGACC  
Class: plasmid ends  
High quality sequence strip: 19.

## FEATURES

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/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ394192 (1-19)

QY 195 ThrLeuGlyLeu 198  
|||||  
DB 7 ACCCTGGGCTTA 18

## RESULT 17

AZ418201 19 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0194M12F Mouse 10kb plasmid U081M library Mus musculus genomic  
DEFINITION clone U081M0194M12 F, genomic survey sequence.

ACCESSION AZ418201  
VERSION AZ418201.1 GI:10542214  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Plate: 0194 row: M column: 12  
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Location/Qualifiers  
1..19

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.48e+05 Length: 19  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0  
US-09-966-880A-8 (1-198) x AZ418201 (1-19)  
QY 162 TTPGUGUYLEU 165  
DB 12 TGGAGGGATTG 1  
RESULT 18  
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LOCUS AZ441188/c  
DEFINITION IM0232004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0232004 R, genomic survey sequence.  
ACCESSION AZ441188  
VERSION AZ441188.1 GI:10565117  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamil, C.,  
Islami, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0232 row: O column: 04  
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Class: plasmid ends  
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Location/Qualifiers  
1..19

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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.48e+05 Length: 19  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0  
US-09-966-880A-8 (1-198) x AZ441188 (1-19)  
QY 60 LEUPHELEUARG 63  
DB 15 CTGTTTAAAGA 4  
RESULT 19  
AZ447414 19 bp DNA linear GSS 04-OCT-2000  
LOCUS AZ447414/c  
DEFINITION IM0244L06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0244L06 R, genomic survey sequence.  
ACCESSION AZ447414  
VERSION AZ447414.1 GI:10599182  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)  
 AUTHORS Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niedermauser,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunm@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0244 row: L column: 06  
 Seg primer: CACACAGGAAACAGCTATGACC  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
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 of pMD42 (g1|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0  
 US-09-966-880A-8 (1-198) x AZ478491 (1-19)  
 QY 23 GIYARGARGGJL 26  
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 |||||  
 DB 19 GGAAGAGGAG 8  
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 |||||  
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 LOCUS AZ478491/c  
 DEFINITION 1M0298P03R Mouse 10kb plasmid U06C1M library Mus musculus genomic  
 clone U06C1M0298P03 R, genomic survey sequence.  
 ACCESSION AZ478491  
 VERSION AZ478491.1 GI:10637389

KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE  
 AUTHORS Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niedermauser,A. and Wright,D.,Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunm@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
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 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0  
 US-09-966-880A-8 (1-198) x AZ478491 (1-19)  
 QY 27 THTTYTLeuCyS 30  
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 DB 15 ACATATTGTGT 4  
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 AZ498063/c

LOCUS AZ498063 19 bp DNA linear GSS 05-OCT-2000  
 DEFINITION 1M033508F Mouse 10kb plasmid tUGC1M library Mus musculus genomic  
 clone tUGC1M033508 F, genomic survey sequence.  
 ACCESSION AZ498063  
 VERSION AZ498063.1 GI:10675575  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weis, R.  
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 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
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 10.5 kb range using preparative agarose gel  
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 of PMD42 (g1[4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
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 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Db |||||  
 15 TCCTTACGATA 4  
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 LOCUS AZ582154  
 DEFINITION 1M0374C19F Mouse 10kb plasmid tUGC1M library Mus musculus genomic  
 clone tUGC1M0374C19 F, genomic survey sequence.  
 ACCESSION AZ582154  
 VERSION AZ582154.1 GI:11700755  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 REFERENCE Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
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 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 electrophoresis. Vector DNA was prepared from a derivative  
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ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0

US-09-966-880A-8 (1-198) x AZ498063 (1-19)  
 Oy 105 SerLeuArgIle 108

DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ595016 (1-19)

QY 39 AlarhSerphe 42  
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 8 GCTACTCTCTTT 19

RESULT 23  
 AZ595016 19 bp DNA linear GSS 13-DEC-2000  
 AZ595016/c  
 LOCUS  
 DEFINITION clone UUGC1M0407C19 F, genomic survey sequence.

ACCESSION  
 AZ595016  
 VERSION  
 AZ595016.1 GI:11717206  
 KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 1 (bases 1 to 19)  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niedermauern, A. and Wright, D., Weisse, R.  
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 Unpublished (2000)

JOURNAL  
 COMMENT  
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 University of Utah  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0407 row: C column: 19  
 Seq primer: CCGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
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 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 of pMD42 (g114732114[gb|AF129072.1]), a copy-number  
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 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ595016 (1-19)

QY 162 TPGIuglyLeu 165  
 |||||  
 17 TCGAGAGGCTG 6

RESULT 24  
 AZ595242 19 bp DNA linear GSS 13-DEC-2000  
 AZ595242/c  
 LOCUS  
 DEFINITION clone UUGC1M0407C15 R, genomic survey sequence.

ACCESSION  
 AZ595242  
 VERSION  
 AZ595242.1 GI:11717432  
 KEYWORDS  
 GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niedermauern, A. and Wright, D., Weisse, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0407 row: C column: 15  
 Seq primer: CACACAGCAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g114732114[gb|AF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ALIGNMENT SCORES:

Score:	4.48e+05	Length:	19
Percent Similarity:	100.00%	Matches:	4
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	2.02%	Mismatches:	0
		Indels:	0
		Gaps:	0

US-09-966-880A-8 (1-198) x AZ595242 (1-19)

Qy 32 VALVALLYARG 35  
14 GTTGTAAACGA 3

RESULT 25  
AZ617087/C

LOCUS 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0448M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0448M12 F, genomic survey sequence.

ACCESSION AZ617087  
VERSION AZ617087.1 GI:11739277

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Niederhauser,A., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhauser,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0448 row: M column: 12  
Seq primer: GGTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
1..19  
/organism="Mus musculus"  
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/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF199072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ALIGNMENT SCORES:

Score:	4.48e+05	Length:	19
Percent Similarity:	100.00%	Matches:	4
Best Local Similarity:	100.00%	Conservative:	0
Query Match:	2.02%	Mismatches:	0
		Indels:	0
		Gaps:	0

US-09-966-880A-8 (1-198) x AZ617087 (1-19)

Qy 149 AanturPheVal 152  
18 AATGCTTTGTC 7

RESULT 26  
AZ661787

LOCUS 19 bp DNA linear GSS 14-DEC-2000  
DEFINITION 1M0540I06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0540I06 R, genomic survey sequence.

ACCESSION AZ661787  
VERSION AZ661787.1 GI:11798933

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Niederhauser,A., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhauser,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE Unpublished (2000)  
JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0540 row: I column: 06  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0540I06"  
/sex="Male"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880a-8 (1-198) x AZ661787 (1-19)

QY 69 AspleuAspPro 72

Db 6 GATCTGATCCC 17

RESULT 27

AZ784061 19 bp DNA linear GSS 16-FEB-2001

LOCUS

DEFINITION 2M0026M20F Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0026M20 F, genomic survey sequence.

ACCESSION AZ784061.1 GI:12919427

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0026 row: M column: 20

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence strop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGM0026M20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880a-8 (1-198) x AZ784061 (1-19)

QY 4 LeuLeuMetAsn 7

Db 15 CTGCTTATGAT 4

RESULT 28

AZ799394 19 bp DNA linear GSS 16-FEB-2001

LOCUS

DEFINITION 2M0056J18R Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0056J18 R, genomic survey sequence.

ACCESSION AZ799394.1 GI:12950467

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: J column: 18

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence strop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UGCGM0056J18"

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/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214[gbl]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

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US-09-966-880A-8 (1-198) x AZ799394 (1-19)

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Oy 91 AlarphVal 94
Db 16 GCAGGCACTTT 5

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## RESULT 29

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AZ834391 19 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0117N04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0117N04 F, genomic survey sequence.
ACCESSION AZ834391
VERSION AZ834391.1 GI:13004299
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0117 row: N column: 04  
Seq primer: CGTGTATAAAGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19

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/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0117N04"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214[gbl]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

```

US-09-966-880A-8 (1-198) x AZ834391 (1-19)

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Oy 107 Argillepethr 110
Db 1 AGGATCTTACC 12

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## RESULT 30

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AZ864551 19 bp DNA linear GSS 21-FEB-2001
LOCUS 2M0174M11F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
DEFINITION clone UUGC2M0174M11 F, genomic survey sequence.
ACCESSION AZ864551
VERSION AZ864551.1 GI:13063965
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

```

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah  
Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0174 row: M column: 11

## FEATURES

## source

Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence scop: 19.  
 Location/Qualifiers

## FEATURES

source

1..19

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCGM library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.48e+05 Length: 19  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ864551 (1-19)

Oy 6 MetaenAARG 9

Db 2 ATGATCGCCG 13

RESULT 31

LOCUS AU013258

DEFINITION AU013258 Schizosaccharomyces pombe late log phase cDNA

ACCESSION AU013258

VERSION AU013258.1 GI:3368049

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

REFERENCE 1 (bases 1 to 20)

AUTHORS Moriyama, M. and Mita, K.

TITLE Identification of expressed sequence tags of Schizosaccharomyces

JOURNAL Unpublished (1998)

COMMENT Contact: Mitsuo Moriyama

FEATURES

source

1..20

/organism="Schizosaccharomyces pombe"  
 /mol\_type="mRNA"  
 /strain="972"  
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 /sex="h minus"  
 /clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

## ORIGIN

## Alignment Scores:

Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AU013258 (1-20)

Oy 3 SerLeuMet 6

Db 2 TCATTACTAATG 13

RESULT 32

LOCUS AU255876/c

DEFINITION AU255876 3'-directed mouse cDNA library Mus musculus cDNA clone

ACCESSION BE00006684 3', mRNA sequence.

VERSION AU255876.1 GI:20319029

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)

AUTHORS Kato, K. and Matoba, R.

TITLE Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished (2002)

COMMENT Contact: Kikuya Kato

Graduate School of Biological Sciences

Nara Institute of Science and Technology

8916-5 Takayama, Ikoma, Nara 630-0101, Japan

Tel: 81-743-72-5581

Fax: 81-743-72-5589

Email: kkatob@nara.ac.jp, URL: <http://love2.aist-nara.ac.jp/BE0/index.html>.

location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="BE00006684"

/tissue\_type="brain"

/clone\_lib="3'-directed mouse cDNA library"

## Alignment Scores:

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 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AU255876 (1-20)

QY 125 G1YLEuAARG 128  
 Db 14 GGCTTAGAAGA 3

RESULT 33  
 LOCUS BX558127  
 DEFINITION BX558127 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans CDNA clone Tse6909.glc, mRNA sequence.

ACCESSION EX558127  
 VERSION EX558127.1 GI:33429274  
 KEYWORDS EST  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Lehane M.J., Aksoy S., Gibson W., Kephornou A., Berriman M., Hamilton J., Soares M.B., Bonaldo M.F., Lehane S. and Hall N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW

FEATURES  
 source  
 1..20  
 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse6909.glc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T. brucei"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BX558127 (1-20)

QY 73 G1YARGVATY 76  
 Db 1 GGAGGTGTAT 12

RESULT 34  
 LOCUS CA851019/c  
 DEFINITION D09C05\_E05\_05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
 CA851019  
 CA851019 20 bp mRNA linear EST 01-AUG-2003  
 VERSION CA851019.1 GI:33387612

KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.  
 TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Alkharouf, N.W.  
 Soybean Genomics and Improvement Laboratory (SGIL)  
 US Department of Agriculture (USDA), ARS, PSI  
 Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA  
 Tel: 301 504 5750  
 Fax: 301 504 5728  
 Email: alkharouf@ars.usda.gov.

FEATURES  
 source  
 1..20  
 Location/Qualifiers  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Peking"  
 /db\_xref="taxon:3847"  
 /clone="D09C05"  
 /tissue\_type="Roots"  
 /dev\_stage="Seedlings"  
 /clone\_lib="cDNA Peking library 2, 4 day SCN3"  
 /note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA851019 (1-20)

QY 41 SerPhaserleu 44  
 Db 18 TCCTTCNTTA 7

RESULT 35  
 LOCUS CF322764/c  
 DEFINITION HDN--02-A02.g1 OSHDAC1-overexpressing transgenic rice lambda phase CDNA library II (HDN) Oryza sativa CDNA clone HDN--02-A02, mRNA sequence.  
 ACCESSION CF322764  
 VERSION CF322764.1 GI:33793762  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
Location/Qualifiers

# FEATURES

source

```
1.20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--02-A02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOL8"
/clone_lib="roshDACI-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

## ORIGIN

### Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score: 4.73e+05	20	4	0
Percent Similarity: 100.00%		0	0
Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 2.02%		Indels: 0	
DB: 14		Gaps: 0	

US-09-966-880a-8 (1-198) x CF327694 (1-20)

QY 170 Valargleuser 173

Db 20 GTTAGGTTGAGT 9

## RESULT 36

CF327699/c

LOCUS

DEFINITION NACL--02-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza

ACCESSION

CF327699.1 GI:33803647

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

```
1.20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
```

## ORIGIN

### Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score: 4.73e+05	20	4	0
Percent Similarity: 100.00%		0	0
Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 2.02%		Indels: 0	
DB: 14		Gaps: 0	

US-09-966-880a-8 (1-198) x CF327699 (1-20)

QY 180 LeuleuProleu 183

Db 15 CTCCTCCCCCTC 4

## RESULT 37

AZ303578/c

LOCUS

DEFINITION 20 bp DNA linear GSS 29-SEP-2000

clone UUGC1M0003H07 F, genomic survey sequence.

ACCESSION

AZ303578

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

```
1.20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0003H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI:4732114|DB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
```

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:	2.02%						
DB:	28						

US-09-966-880A-8 (1-198) x AZ307763 (1-20)

QY 62 LeuAqTyrile 65  
15 CTCAGATATATA 4

RESULT 38  
AZ307763 20 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0010F06F Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0010F06 F, genomic survey sequence.  
ACCESSION AZ307763  
VERSION AZ307763.1 GI:10347078  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0010 row: F column: 06  
Seq primer: CATTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

## FEATURES

source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0010F06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/vector="PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (41473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:	2.02%						
DB:	28						

US-09-966-880A-8 (1-198) x AZ307763 (1-20)

QY 172 LeuSerArgGln 175  
20 CTCACAGACAA 9

RESULT 39  
AZ331739 20 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0059D21R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0059D21 R, genomic survey sequence.  
ACCESSION AZ331739  
VERSION AZ331739.1 GI:10394723  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0059 row: D column: 21  
Seq primer: CACACAGCAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

## FEATURES

source

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UGCGM0059D21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGCGM library"  
/vector="PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The sheared DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	4.00	100.00%	100.00%	2.02%	20	4	0	0	0	0

US-09-966-880A-8 (1-198) x AZ331739 (1-20)

QY 27 ThryLeuQys 30

DB 12 ACTATTATGT 1

RESULT 40

AZ348201

LOCUS 20 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0084F13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ348201

VERSION AZ348201.1 GI:10427438

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niedermauser,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0084 row: F column: 13

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0084F13"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

## ORIGIN

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	4.00	100.00%	100.00%	2.02%	20	4	0	0	0	0

US-09-966-880A-8 (1-198) x AZ348201 (1-20)

QY 125 G1yleuArgArg 128

DB 5 GCACGTGAGGAGA 16

RESULT 41

AZ387854/c

LOCUS 20 bp DNA linear GSS 02-OCT-2000

DEFINITION 1M0147K24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ387854

VERSION AZ387854.1 GI:10501562

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niedermauser,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0147 row: K column: 24

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0147K24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1b="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42m; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ387854 (1-20)

Qy 151 PheValGluAsn 154  
 Db 15 TTGTGTAATAAT 4

## RESULT 42

AZ400362

LOCUS

DEFINITION 1M0166C1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0166C11 R, genomic survey sequence.

ACCESSION AZ400362.1 GI:10515436

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)

JOURNAL

COMMENT

Contract: Robert B. Weiss  
 University of Utah  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0166 row: C column: 11  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends

FEATURES  
 source  
 High quality sequence stop: 20.  
 Location/Qualifiers  
 1..20

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0166C11"  
 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_1b="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42m; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ400362 (1-20)

Qy 179 IleLeuLeuPro 182  
 Db 6 ATTITGTCGA 17

## RESULT 43

AZ408559

LOCUS

DEFINITION 1M0179K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0179K14 R, genomic survey sequence.

ACCESSION AZ408559

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)

JOURNAL

COMMENT

Contract: Robert B. Weiss  
 University of Utah  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0179 row: K column: 14

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0179K14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ486559 (1-20)

QY 194 ArgThrLeuGly 197

DB 7 AGGACACTGGGG 18

## RESULT 44

AZ486007

LOCUS

DEFINITION IM0313B17R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0313B17 R, genomic survey sequence.

ACCESSION

AZ486007

VERSION AZ486007.1 GI:10652355

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0313 row: E column: 17

Seq primer: CACACAGGAAACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

## FEATURES

source

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/mol\_type="genomic DNA"

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/clone="UUC1M0313B17"

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

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Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ486007 (1-20)

QY 180 LeuLeuProLeu 183

DB 4 CTCTGCCCTC 15

## RESULT 45

AZ489135

LOCUS

DEFINITION IM0319H15R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0319H15 R, genomic survey sequence.

ACCESSION

AZ489135

VERSION AZ489135.1 GI:10658589

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

University of Utah Genome Center

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Class: plasmid ends  
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/strain="C57BL/6J"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PMD42hv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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electrophoresis. Vector DNA was prepared from a derivative  
of PMD42 (g1[4732114]gb[AF129072.1]) a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0  
US-09-966-880A-8 (1-198) x AZ489135 (1-20)

QY 97 PheLeuAArgGly 100  
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Db 8 TTTCTGAGGGGA 19

RESULT 46  
AZ630786 20 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0484U01R Mouse 10kb plasmid UGCM library Mus musculus genomic  
DEFINITION clone UGCM1M0484U01 R, genomic survey sequence.  
ACCESSION AZ630786  
VERSION AZ630786.1 GI:11752976  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (baees 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhuesern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0484 row: J column: 01  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/organism="Mus musculus"  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UTGCM0484U01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1ib="Mouse 10kb plasmid UGCM library"  
/note="Vector: PMD42hv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0  
US-09-966-880A-8 (1-198) x AZ630786 (1-20)

QY 186 ValAspAspLeu 189  
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Db 5 GTTGATGATCTC 16

RESULT 47  
AZ650507 20 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0520A16R Mouse 10kb plasmid UGCM library Mus musculus genomic  
DEFINITION clone UGCM1M0520A16 R, genomic survey sequence.  
ACCESSION AZ650507  
VERSION AZ650507.1 GI:11785064

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
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Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0520 row: A column: 16  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends

FEATURES  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ650507 (1-20)

QY 108 llePheThrAla 111  
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3 ATCTTACAGCA 14

RESULT 48  
AZ762322/c

LOCUS AZ762322 20 bp DNA linear GSS 16-FEB-2001

DEFINITION 1M0557G12P Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0557G12 F, genomic survey sequence.

ACCESSION AZ762322

VERSION AZ762322.1 GI:12872206

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0557 row: G column: 12  
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Class: plasmid ends

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ762322 (1-20)

QY 59 leuLeuPheLeu 62

Db 19 CTAATTCTG 8

RESULT 49  
A2772787/c  
LOCUS  
DEFINITION 20 bp DNA linear GSS 16-FEB-2001  
1M0583M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0583M24 R, genomic survey sequence.

ACCESSION  
A2772787  
VERSION  
A2772787.1 GI:12896465  
KEYWORDS  
GSS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
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JOURNAL  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0583 row: M column: 24  
Seq primer: CACACAGAAACAGCTATGACC  
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/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
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Query Match: 2.02% Indels: 0

DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x A2772787 (1-20)

Qy 60 Leupheleuarg 63  
Db 17 TTAATCTTAAAG 6

RESULT 50  
A2775696  
LOCUS  
DEFINITION 20 bp DNA linear GSS 16-FEB-2001  
2M0008K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0008K09 R, genomic survey sequence.

ACCESSION  
A2775696  
VERSION  
A2775696.1 GI:12902501  
KEYWORDS  
GSS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
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plasmid inserts

TITLE  
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JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0008 row: M column: 09  
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High quality sequence stop: 20.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0008K09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
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ORIGIN  
Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0

Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x A2775696 (1-20)

Qy 103 AenLuserLew 106  
 Db 2 AATCTATCTTA 13

RESULT 51  
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 LOCUS A2776071/c  
 DEFINITION 2M0009124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0009124 F, genomic survey sequence.

ACCESSION A2776071  
 VERSION A2776071.1 GI:12903267  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
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 84112, USA  
 TEL: 801 585 5606  
 FAX: 801 585 7177  
 EMAIL: ddunn@genetics.utah.edu  
 INSERT LENGTH: 10000 Std Error: 0.00  
 PLATE: 0009 ROW: 1 COLUMN: 24  
 SEQ PRIMER: CGTTGTAAACGACGCGCAGT  
 CLASS: plasmid ends  
 HIGH QUALITY SEQUENCE STOP: 20.  
 Location/Qualifiers  
 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0009124"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD29; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapter mouse DNA was annealed to  
 adapter vector DNA, and transformed into

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.73e+05 Length: 20  
 Score: 4.00 Matches: 4  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 2.02% Indels: 0  
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x A2776071 (1-20)

Qy 126 LeuArgArgLew 129  
 Db 14 CTTGCAAGCTTA 3

RESULT 52  
 A2810573 20 bp DNA linear GSS 20-FEB-2001  
 LOCUS A2810573  
 DEFINITION 2M0076K11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0076K11 F, genomic survey sequence.

ACCESSION A2810573  
 VERSION A2810573.1 GI:12977957  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 UNIVERSITY of Utah Genome Center  
 RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 TEL: 801 585 5606  
 FAX: 801 585 7177  
 EMAIL: ddunn@genetics.utah.edu  
 INSERT LENGTH: 10000 Std Error: 0.00  
 PLATE: 0076 ROW: K COLUMN: 11  
 SEQ PRIMER: CGTTGTAAACGACGCGCAGT  
 CLASS: plasmid ends  
 HIGH QUALITY SEQUENCE STOP: 20.  
 Location/Qualifiers  
 1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0076K11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /note="Vector: PMD29; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapter DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	100.00%	0	0	0
Percent Similarity:		100.00%						
Best Local Similarity:		100.00%						
Query Match:		2.02%						
DB:	28							

US-09-966-880A-8 (1-198) x AZ810573 (1-20)

QY 6 MetAmpArg 9

DB 1 ATGAATCGCCG 12

## RESULT 53

AZ832946

LOCUS 2M0113M1R Mouse 10kb plasmid UGCGM library Mus musculus genomic

DEFINITION clone UGCG2M0113M1 R, genomic survey sequence.

ACCESSION AZ832946

VERSION AZ832946.1 GI:13002854

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

UNIVERSITY OF UTAH

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0113 row: M column: 11

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence strop: 20.

Location/Qualifiers

## FEATURES

source

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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0113M1"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

## ORIGIN

## Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Best Local Similarity:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	100.00%	0	0	0
Percent Similarity:		100.00%						
Best Local Similarity:		100.00%						
Query Match:		2.02%						
DB:	28							

US-09-966-880A-8 (1-198) x AZ832946 (1-20)

QY 102 ProAmpLeuSer 105

DB 2 CCTAACCTCTCT 13

## RESULT 54

AZ834080

LOCUS 2M0116A09R Mouse 10kb plasmid UGCGM library Mus musculus genomic

DEFINITION clone UGCG2M0116A09 R, genomic survey sequence.

ACCESSION AZ834080

VERSION AZ834080.1 GI:13003988

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH GENOME CENTER

UNIVERSITY OF UTAH

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0116 row: A column: 09

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence strop: 20.

Location/Qualifiers

## FEATURES

source

1..20  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0116A09"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ834080 (1-20)

QY 59 LeuLeuPheLeu 62  
|||||  
5 TTGCTCTTCTA 16

## RESULT 55

AZ949545 20 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0213E19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0213E19 F, genomic survey sequence.

ACCESSION AZ949545

VERSION AZ949545.1 GI:13820772

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.

AUTHORS

TITLE plasmid inserts scaffolding with paired end reads from 10kb

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0213 Row: E Column: 19  
Seq primer: CGTGTAAACAGACGCCAGT  
Class: Plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
source 1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0213E19"

/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1b="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: pMD42uv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The digested DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Alignment Scores:  
Pred. No.: 4.73e+05 Length: 20  
Score: 4.00 Matches: 4  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.02% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ949545 (1-20)

QY 172 LeuSerArgGln 175  
|||||  
9 CTCTCTAGACAG 20

## RESULT 56

CA853358 9 bp mRNA linear EST 01-AUG-2003  
LOCUS B07D03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone  
DEFINITION B07D03 5', mRNA sequence.

ACCESSION CA853358

VERSION CA853358.1 GI:33390151

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 9)  
Alkharouf,N.W., Khan,R. and Matthews,B.F.  
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
Unpublished (2002)  
Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA  
Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharouf@ars.usda.gov.  
Location/Qualifiers

FEATURES  
source 1..9  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
/clone="B07D03"  
/issue\_type="Roots"

ORIGIN

/dev\_stage="Seedlings"  
/clone\_lib="CDNA Peking library 12hr SCN3"  
/note="vector: pBluescript SK-; cDNA clones from mRNA  
extracted from roots of soybean cv. Peking 12 hrs after  
infection by SCN race 3. These are cloned in pBluescript  
SK- phagemid."

## Alignment Scores:

Pred. No.: 5.5e+07 Length: 9  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservatve: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA853358 (1-9)

QY 40 Therserpe 42

DB 9 ACNAGCTTT 1

RESULT 57

HSN004456/c standard; mRNA; EST; 10 BP.

ID HSN004456

AC AL039980;

XX AL039980.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434J1012\_r1 (from clone DKFZp434J1012)

DE Homo sapiens mRNA; EST DKFZp434J1012\_r1 (from clone DKFZp434J1012)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MFS, Am Klopferstutz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by Qiagen within the CDNA

CC sequencing consortium of the German Genome Project

CC No. 81 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key

XX Location/Qualifiers

XX source

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSN004456 (1-10)

QY 193 Pharygthr 195

DB 9 TTCGGAGCC 1

RESULT 58

HSN005384/c standard; mRNA; EST; 10 BP.

ID HSN005384

AC AL040908;

XX AL040908.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434J1415\_g1 (from clone DKFZp434J1415)

DE Homo sapiens mRNA; EST DKFZp434J1415\_g1 (from clone DKFZp434J1415)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Bloeker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MFS, Am Klopferstutz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by GBF within the CDNA

CC sequencing consortium of the German Genome Project

CC No. 81 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key

XX Location/Qualifiers

XX source

XX 1.10

XX /db\_xref="taxon:9606"

XX /mol\_type="mRNA"

XX /organism="Homo sapiens"

XX /clone\_lib="434 (synonym: hhes3). Vector pSport1; host

XX DH10B; sites NotI + SalI

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSN005384 (1-10)

QY 105 Serleung 107

DB 10 AGCTTAGCT 2

RESULT 59

CF313993/c

HSN005384/c standard; mRNA; EST; 10 BP.

ID HSN005384

AC AL040908;

XX AL040908.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434J1415\_g1 (from clone DKFZp434J1415)

DE Homo sapiens mRNA; EST DKFZp434J1415\_g1 (from clone DKFZp434J1415)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]

RA Bloeker H., Boecker M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MFS, Am Klopferstutz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by GBF within the CDNA

CC sequencing consortium of the German Genome Project

CC No. 81 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key

XX Location/Qualifiers

XX source

XX 1.10

XX /db\_xref="taxon:9606"

XX /mol\_type="mRNA"

XX /organism="Homo sapiens"

XX /clone\_lib="434 (synonym: hhes3). Vector pSport1; host

LOCUS CF313993 10 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--02-F15.b1 OSHDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-F15, mRNA sequence.  
 ACCESSION CF313993  
 VERSION CF313993.1 GI:33685754  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..10  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD--02-F15"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO, site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.07e+06 Length: 10  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF313993 (1-10)  
 QY 23 GYARGARG 25  
 Db 10 GGCCGACGG 2  
 RESULT 60  
 CF323895 10 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF323895  
 DEFINITION HDN--05-A22.g1 OSHDACL-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA sequence.  
 ACCESSION CF323895  
 VERSION CF323895.1 GI:33796055  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..10  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HDN--05-A22"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"  
 /note="Vector: pBluescript SK(+); site 1: EcoRI; site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.07e+06 Length: 10  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF323895 (1-10)  
 QY 123 PROGLUGLY 125  
 Db 2 CCCGACGC 10  
 RESULT 61  
 CF339022 10 bp mRNA linear EST 18-AUG-2003  
 LOCUS CF339022/c  
 DEFINITION RCL1--03-117.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-117, mRNA sequence.  
 ACCESSION CF339022  
 VERSION CF339022.1 GI:33826427  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 10)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..10  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"

```

/clone="RCL1-03-117"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/notes="Vector: pBluescript SK(+); Site 1: SacI; Site 2: XhoI. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SacI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

```

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2-07e+06	3.00	100.00%	100.00%	1.52%	10	3	0	0	0	0

US-09-966-880a-8 (1-198) x CF339022 (1-10)

OY 43 SerLeuASP 45  
 10 TCTCTAGAT 2

## RESULT 62

HSN008167/c  
 ID HSN008167 standard; mRNA; EST: 11 BP.

AC AL043317;  
 XX SV AL043317.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434N0723\_r1 (from clone DKFZp434N0723)

XX KM EST: expressed sequence tag.

XX OS Homo sapiens (human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX

RN [1]  
 RP 1-11  
 RA Blum H., Bauersachs S., Mewes W., Gaassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Kiopterpeitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the cDNA

CC sequencing consortium of the German Genome Project

CC No s1 sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1.11  
 FT /db\_xref="taxon:9606"  
 FT /mol\_type="mRNA"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="DKFZp434N0723"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSPORT1; host  
 FT DH10B; sites NotI + SalI  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"

XX Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 other;

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.29e+06	3.00	100.00%	100.00%	1.52%	11	3	0	0	0	0

US-09-966-880a-8 (1-198) x HSN008167 (1-11)

OY 193 PheArgThr 195  
 9 TTCGAGAC 1

## RESULT 63

BG896271  
 LOCUS BG896271 11 bp mRNA linear EST 06-NOV-2001

DEFINITION H0A28-1-G6 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,

ACCSSION BG896271 GI:14306512

VERSION BG896271.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Kumar,S., Connor,J.R., Dodde,R.A., Halsey,W., Van Horn,M., Mao,J.,

Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M., and

Lark,M.W. Identification and initial characterization of 5000 expressed

sequence tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

JOURNAL MEDLINE 21482651

PUBMED 11597177

COMMENT Contact: Sanjay Kumar

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com

Seq primer: T7.

FEATURES Location/Qualifiers

1.11 /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="cartilage"

/lab\_host="E.coli DH10 B"

/clone\_lib="HOA (Human Osteoarthritic Cartilage)"

/notes="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2.29e+06	3.00	100.00%	100.00%	1.52%	11	3	0	0	0	0

US-09-966-880a-8 (1-198) x BG896271 (1-11)

OY 111 AlaArgLeu 113

DB 3 GCCGAGAC 11

## RESULT 64

BG927412/c

LOCUS BG927412 11 bp mRNA linear EST 06-NOV-2001  
 DEFINITION HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 ACCESSION BG927412  
 VERSION BG927412.1 GI:14321935  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 11)  
 REFERENCE Kumar,S., Connor,J.R., Dadds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathie,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Latk,M.W.  
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE  
 PUBMED 21482651  
 11597177  
 COMMENT Contact: Sanjay Kumar  
 UM2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-1@sk.com  
 Seq primer: 77.  
 FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="Hs.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1, Site\_1: SalI; Site\_2: NotI; Directional"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.29e+06 Length: 11  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880A-8 (1-198) x BG927412 (1-11)  
 QY 132 AAGAGYVal 134  
 |||||  
 10 GCTGGCGTA 2  
 RESULT 65  
 BM395226/c 11 bp mRNA linear EST 17-JAN-2002  
 LOCUS 50072-2-8-B04.f.2 Chilcoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM395226  
 VERSION BM395226.1 GI:18195279  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
 1 (bases 1 to 11)  
 REFERENCE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
 Turkewiz,A.P. and Klobutcher,L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 JOURNAL Contact: Turkewitz AP  
 COMMENT Molecular Genetics and Cell Biology

University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: 73.  
 FEATURES  
 source Location/Qualifiers  
 1..11  
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 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
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 Alignment Scores:  
 Pred. No.: 2.29e+06 Length: 11  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880A-8 (1-198) x BM395226 (1-11)  
 QY 38 SerAlaThr 40  
 |||||  
 10 AGCGCCACA 2  
 RESULT 66  
 BM395984/c 11 bp mRNA linear EST 17-JAN-2002  
 LOCUS 5009-0-15-C03.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM395984  
 VERSION BM395984.1 GI:18196037  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
 1 (bases 1 to 11)  
 REFERENCE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 JOURNAL Contact: Turkewitz AP  
 COMMENT Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: 73.  
 FEATURES  
 source Location/Qualifiers  
 1..11  
 /organism="Tetrahymena thermophila"  
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 /strain="CU428.1"  
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 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
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 Alignment Scores:  
 Pred. No.: 2.29e+06 Length: 11  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880a-8 (1-198) x BM3595984 (1-11)

QY 38 SerA1atnr 40  
 DB 11 TCCGCCACC 3

RESULT 67  
 BQ587100 11 bp mRNA linear EST 06-DEC-2002  
 LOCUS E012350-024-011-122-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
 DEFINITION 024-011-122 5-PRIME, mRNA sequence.  
 ACCESSION BQ587100.1 GI:26116682  
 VERSION BQ587100.1  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 11)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaa@mpiz-koeln.mpg.de  
 Insert Length: 11 Std Error: 0.00  
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 Location/Qualifiers  
 1..11  
 /organism="Beta vulgaris"  
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 /clone="024-011-122"  
 /tissue\_type="leaf"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-leaf"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany; contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.29e+06 Length: 11  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ587100 (1-11)

QY 181 LeuProLeu 183  
 DB 2 TTACCTTG 10

RESULT 68  
 BQ595495 11 bp mRNA linear EST 06-DEC-2002  
 LOCUS E012691-024-022-014-SP6 MP12-ADIS-024-developing root Beta vulgaris  
 DEFINITION cDNA clone 024-022-014 5-PRIME, mRNA sequence.  
 ACCESSION BQ595495  
 VERSION BQ595495.1 GI:26125078  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 11)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaa@mpiz-koeln.mpg.de  
 Insert Length: 11 Std Error: 0.00  
 Plate: 11 row: 0 column: 14  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
 Location/Qualifiers  
 1..11  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KMS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:191359"  
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 /clone="024-022-014"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KMS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany; contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.29e+06 Length: 11  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ595495 (1-11)

QY 181 LeuProLeu 183  
 DB 2 TTACCTTG 10

Db 1 CTCCTT 9

RESULT 69  
CF339065/c 11 bp mRNA linear EST 18-AUG-2003

LOCUS  
DEFINITION RC11--03-K22.g1 Regenerated callus lambda phage cDNA library (RC11)

ACCESSION  
CF339065  
ORYZA SATIVA cDNA clone RC11--03-K22, mRNA sequence.

VERSION  
CF339065.1 GI:33826512

KEYWORDS  
EST.

SOURCE  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Zingiberaceae; Oryzae; Oryza.

REFERENCE  
1 (bases 1 to 11)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

COMMENT  
Contact: Nam B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..11  
location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
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/note="Vector: pBluescript SK(+); Site 1: SclI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with SclI and 3' end with XhoI site. Callus was  
induced on 2N6 media for 30 days and cultured for 36hrs on  
regenerated media"

ORIGIN  
Alignment Scores:  
Pred. No.: 2.29e+06 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 0  
DB: 14

US-09-966-880A-8 (1-198) x CF339065 (1-11)

QY 38 SerAlaThr 40  
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10 AGTGCACCC 2

RESULT 70  
CF543159 11 bp mRNA linear EST 22-SEP-2003

LOCUS  
DEFINITION S014678-024-030-006-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

ACCESSION  
CF543159  
ORYZA SATIVA cDNA clone S014678-024-030-006-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

VERSION  
CF543159.1 GI:34891599

KEYWORDS  
EST.

SOURCE  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
1 (bases 1 to 11)  
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wnuck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radcliff,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J 32 (5), 845-857 (2002)

JOURNAL  
MEDLINE  
PUBMED  
22352189  
12472698

COMMENT  
Contact: Weishaar B.  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert length: 11 Std Error: 0.00  
Plate: 30 row: 0 column: 06  
Seq primer: SP6.

FEATURES  
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/mol\_type="mRNA"  
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/db\_xref="GABI:936619"  
/db\_xref="taxon:161934"  
/clone="024-030-006"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MP12-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SalI-CCACGCTCCG-Sp1-CC-NotI-77; Note:  
Sequencing granted in the context of the GABI-beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN  
Alignment Scores:  
Pred. No.: 2.29e+06 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 14  
DB: 14

US-09-966-880A-8 (1-198) x CF543159 (1-11)

QY 149 AsnThrPhe 151  
|||||  
1 AACACTTTC 9

RESULT 71  
BH129987 11 bp DNA linear GSS 23-JUL-2001

LOCUS  
DEFINITION G-663.F Maize Random Small-insert Genomic Library Zea mays genomic

ACCESSION  
BH129987  
ZEAMAYS cDNA clone G-663 both, genomic survey sequence.

VERSION  
BH129987.1 GI:14998894

KEYWORDS  
GSS.

SOURCE  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE  
1 (bases 1 to 11)  
Weyers,B.C., Tinney,S.V. and Morgante,M.  
Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome

JOURNAL  
MEDLINE  
21475670  
PUBMED  
11591643  
COMMENT  
Contact: Morgante M  
Suite 200

Genome Res. 11 (10), 1660-1676 (2001)  
21475670  
11591643  
Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M3unitv  
Class: shotgun.

# FEATURES

source  
1.11  
/organism="Zea mays"  
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/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: PCR-Script; Total genomic DNA was  
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## ORIGIN

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Pred. No.: 2.29e+06 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x BH129987 (1-11)

Qy 195 Thrleugly 197

Db 2 ACCCTCGGA 10

RESULT 72  
BH129987/c 11 bp DNA linear GSS 23-JUL-2001  
LOCUS  
DEFINITION  
G-663.F Maize Random Small-insert Genomic Library Zea mays genomic  
clone G-663 both, genomic survey sequence.

ACCESSION  
BH129987  
VERSION  
BH129987.1 GI:14998894  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoidae; Andropogoneae; Zea.  
1 (bases 1 to 11)  
Meyers,B.C., Tingey,S.V. and Morgante,M.  
Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome  
Genome Res. 11 (10), 1660-1676 (2001)  
21475670  
11591643

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com

Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M3unitv  
Class: shotgun.  
Location/Qualifiers  
1.11  
/organism="Zea mays"  
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/clone="G-663"  
/sex="hermaphrodite"  
/tissue\_type="leaf"  
/cell\_type="young leaf"  
/dev\_stage="seedling"  
/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: PCR-Script; Total genomic DNA was  
nebulized; ends were polished with Pfu polymerase and the  
fragments cloned into PCR-Script."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.29e+06 Length: 11  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x BH129987 (1-11)

Qy 98 Leuargly 100

Db 11 CTCGAGG 3

RESULT 73  
HSM007936/c standard; mRNA; EST; 12 BP.  
ID HSM007936  
XX  
AC AL043086;  
XX  
SV AL043086.1

XX 12-MAR-1999 (Rel. 59, Created)  
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
XX

DE Homo sapiens mRNA; EST DKFZp434B0723\_r1 (from clone DKFZp434B0723)

XX EST; expressed sequence tag.

XX Homo sapiens (human)  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]  
RP Blum H., Bauerachs S., Mewes W., Gassenhuber J., Wiemann S.;  
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
RL MIPS, Am Klipferspitz 18a D-82152 Martinsried, GERMANY

XX clone from S. Wiemann, sequenced by LMU within the CDNA  
CC sequencing consortium of the German Genome Project  
CC No st sequence available  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers  
FH source 1.12  
FT /db\_xref="taxon:9606"  
FT

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FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_id="BXKZP44B0723"
FT      /clone_lib="43" (synonym: htes3). Vector pSPORT1, host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
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SQ      Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:      2.51e+06      Length:      12
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:            2              Gaps:        0

US-09-966-880A-8 (1-198) x HSM007936 (1-12)

QY      193 Pheargthr 195
Db      10 TTCGCGACC 2

RESULT 74
LOCUS   BG925521      12 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
ACCESSION BG925521
VERSION   BG925521.1 GI:14320044
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  1 (bases 1 to 12)
  Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
  Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
  Lark,M.W.
  Identification and initial characterization of 5000 expressed
  sequenced tags (ESTs) each from adult human normal and
  osteoarthritic cartilage cDNA libraries
  Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  11597177
  JOURNAL MEDLINE 21482651
  PUBMED 11597177
  COMMENT  Contact: Sanjay Kumar
  UW2109
  GlaxoSmithKline
  709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
  Tel: 610-270-7245
  Fax: 610-270-5598
  Email: sanjay.kumar-1@sk.com
  Seq primer: 17.
  Location/Qualifiers
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  1..12
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  /mol_type="mRNA"
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  /lab_host="E.coli DH10 B"
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  /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
  Directional"

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US-09-966-880A-8 (1-198) x BG925521 (1-12)

QY      181 LeuProLeu 183
Db      3 CTTCCCTC 11

RESULT 75
LOCUS   BQ587766      12 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION BQ12340-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-010-M01 5-PRIME, mRNA sequence.
ACCESSION BQ587766
VERSION   BQ587766.1 GI:26117348
KEYWORDS  EST.
SOURCE    Beta vulgaris
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Caryophyllales; Amaranthaceae; Beta.
  1 (bases 1 to 12)
  Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
  Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
  and Radloff,U.
  Construction of a 'unigene' cDNA clone set by oligonucleotide
  fingerprinting allows access to 25 000 potential sugar beet genes
  Plant J. 32 (5), 845-857 (2002)
  22362189
  JOURNAL MEDLINE 12472698
  PUBMED 12472698
  COMMENT  Contact: Weishaar B
  ADIS DNA core facility at MP1Z
  Max-Planck-Institute for Plant Breeding Research
  Carl-von-Linne Weg 10, 50829 Koeln, Germany
  Fax: 00492215062851
  Email: weishaar@mpiz-koeln.mpg.de
  Insert length: 12 Std Error: 0.00
  Place: 10 Row: 10 column: 01
  Seq primer: SP6; CATACGATTATGATGACACTATAG.
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  /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
  cDNA library from sugar beet, library provided by KWS
  Kleinfeldbener Saatgut AG Rimbach, Germany, contract:
  b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
  orientation:
  SP6-Sall-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
  Sequencing granted in the context of the GABI-Beet
  Project, local PI: Dr. Katharina Schneider, coordinator:
  Prof. Christian Jung, Sequence submission managed by
  RZPD/GABI-Primary database: http://gabi.rzpd.de"

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ORIGIN
Alignment Scores:
Pred. No.:      2.51e+06      Length:      12
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:            13              Gaps:        0

US-09-966-880A-8 (1-198) x BQ587766 (1-12)

QY      3 SerLeuLeu 5

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DB 2 TCTCTCTC 10

RESULT 76  
LOCUS BQ587766/c 12 bp mRNA linear EST 06-DEC-2002  
DEFINITION B01340-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
ACCESSION BQ587766  
VERSION BQ587766.1 GI:26117348  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruock, W., Menze, A., O'Brien, J., Lehnach, H. and Radelof, U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant U. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT  
CONTACT: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mplz-koeln.mpg.de  
Insert length: 12 Std Error: 0.00  
Plate: 10 row: M column: 01  
Seq primer: SP6: CATGCAATTAGGTGACACTATAG.  
Location/Qualifiers

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/note="Vector: PCMVSPORT6; Site\_1: SalI; Site\_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfeldleber Saatzucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-77; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:  
Pred. No.: 2.51e+06 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ587766 (1-12)

QY 24 ArgArgGlu 26  
|||||  
9 AGGAGAG 1

DB  
RESULT 77

BQ750930  
LOCUS BQ750930 12 bp mRNA linear EST 18-JUL-2002  
DEFINITION EST631493 DSCT Colletotrichum trifolii cDNA clone pDSCT1-51, mRNA sequence.  
ACCESSION BQ750930  
VERSION BQ750930.1 GI:21906335  
KEYWORDS EST  
SOURCE Colletotrichum trifolii  
ORGANISM Colletotrichum trifolii  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

REFERENCE  
AUTHORS Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F., and Fraser, C.M.  
TITLE ESTs from mycelia of Colletotrichum trifolii race 1  
JOURNAL Unpublished (2002)  
COMMENT Other ESTs: EST631492  
CONTACT: Deborah A. Samac  
Department of Plant Pathology  
University of Minnesota  
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debby@puccini.crl.umn.edu  
WWW sequence name: MTSAS1rv More information is available at: [www.medicago.org](http://www.medicago.org)  
Seq primer: (pBA ABA CGA CTC ACT ABA 999 C).  
Location/Qualifiers

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/lab\_host="DH5alpha"  
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ORIGIN

Alignment Scores:  
Pred. No.: 2.51e+06 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ750930 (1-12)

QY 119 ArgGlySer 121  
|||||  
4 CGAAGGCC 12

DB  
RESULT 78  
LOCUS BQ750930/c 12 bp mRNA linear EST 18-JUL-2002  
DEFINITION EST631493 DSCT Colletotrichum trifolii cDNA clone pDSCT1-51, mRNA sequence.

ACCESSION BQ750930  
 VERSION BQ750930.1 GI:21906335  
 KEYWORDS EST  
 SOURCE Colletotrichum trifolii  
 ORGANISM Colletotrichum trifolii  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae; Mitosporic Phyllochoraceae; Colletotrichum.  
 1 (bases 1 to 12)  
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uterback,T., Cheung,F. and Fraser,C.M.  
 ESTs from mycelia of Colletotrichum trifolii race 1  
 Unpublished (2002)  
 Other ESTs: EST631492  
 Contact: Deborah A. Samac  
 Department of Plant Pathology  
 University of Minnesota  
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
 Tel: 612 625 1243  
 Fax: 651 649 5058  
 Email: debbysepucini.crl@umn.edu  
 TIGR sequence name: MTSAS11V More information is available at:  
 www.medicago.org  
 Seq primer: (qta Ata CGA CTC ACT Ata ggg C).  
 Location/Qualifiers  
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 /lab\_host="DH5alpha"  
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 /note="Vector: pBluescript SK+, Site\_1: EcoRI, Site\_2: EcoRI, isolate: 2SP2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gII from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,51e+06 Length: 12  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880a-8 (1-198) x BQ750930 (1-12)  
 QY 192 Alaphaarg 194  
 Db 11 GCCTTCGT 3  
 RESULT 79  
 C51419 12 bp mRNA EST 11-SEP-1997  
 C51419/c clone yk195e11 3', mRNA sequence.  
 LOCUS C51419  
 DEFINITION C51419 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA  
 VERSION C51419.1 GI:2389176  
 KEYWORDS EST.  
 SOURCE Caenorhabditis elegans

ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Pelodetinae; Caenorhabditis.  
 1 (bases 1 to 12)  
 Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.  
 Expression map of the C.elegans genome  
 Unpublished (1996)  
 Contact: Yuji Kohara  
 Genome Biology Lab.  
 National Institute of Genetics  
 Yata 1111, Mishima, Shizuoka 411, Japan  
 Tel: 81-559-81-6854  
 Fax: 81-559-81-6855  
 Email: ykoha@lab.nig.ac.jp.  
 Location/Qualifiers  
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ORIGIN  
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 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880a-8 (1-198) x C51419 (1-12)  
 QY 106 leuargile 108  
 Db 12 CTGGCTATA 4  
 RESULT 80  
 CF300273 12 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--04-J19.91 Rice leaf plasmid CDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--04-J19, mRNA sequence.  
 ACCESSION CF300273  
 VERSION CF300273.1 GI:33672034  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 12)  
 Song,S.I., Kim,J.K., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Kim,J.S., Jun,K.M., Cheong,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.  
 Location/Qualifiers  
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FEATURES  
 source

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 113 LeuTYTPhe 115

Db 11 TTATATTTT 3

RESULT 81

CF311969 12 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

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/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 113 LeuTYTPhe 115

Db 11 TTATATTTT 3

RESULT 81

CF311969 12 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 172 LeuSerArg 174

Db 2 CTGTCAAGA 10

RESULT 82

CF311969/c 12 bp mRNA linear EST 15-AUG-2003

LOCUS ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-H13, mRNA sequence.

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 36 ArgAspSer 38

Db 9 CGTGACAGC 1

RESULT 83

CF329021/c 12 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--04-D03.g1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa cDNA clone NACL--04-D03, mRNA sequence.

ACCESSION CF329021

VERSION CF329021.1 GI:33806279  
 EST.  
 KEYWORDS  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 12)  
 REFERENCE  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..12  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="NACL--04-D03"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.51e+06 Length: 12  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF329021 (1-12)

QY 59 leu|eu|phe 61  
 |||||  
 12 TTTATTTT 4

RESULT 84  
 CF331951/c 12 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--08-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--08-E07, mRNA sequence.  
 ACCESSION CF331951  
 VERSION CF331951.1 GI:33812123  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 12)  
 REFERENCE  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Jun,K.M., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..12  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="NACL--08-E07"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.51e+06 Length: 12  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF331951 (1-12)

QY 11 Phe|eu|tyr 13  
 |||||  
 12 TTTTATAT 4

RESULT 85  
 AQ03019 12 bp DNA linear GSS 09-JUN-2001  
 LOCUS GSSC07904 Trypanosoma cruzi random genomic library Trypanosoma  
 DEFINITION cruzi genomic clone G35A7, genomic survey sequence.  
 ACCESSION AQ03019.2 GI:9375801  
 VERSION AQ03019.2  
 KEYWORDS GSS.  
 SOURCE Trypanosoma cruzi  
 ORGANISM Trypanosoma cruzi  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.  
 1 (bases 1 to 12)  
 REFERENCE  
 AUTHORS Agüero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.  
 TITLE A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery  
 JOURNAL Genome Res. 10 (12), 1996-2005 (2000)  
 MEDLINE 20568489  
 PUBMED 11116094  
 COMMENT On Jul 21, 2000 this sequence version replaced gi:6478057.  
 Contact: Sanchez D.O.  
 Instituto de Investigaciones Biotecnológicas (Univ. Nac. de Gral San Martín)  
 Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martín, Buenos Aires, Argentina  
 Tel: (54-11) 4580/7255/7  
 Fax: (54-11) 4752-9639  
 Email: dsanchez@ib.unsam.edu.ar  
 Seq primer: T7  
 Class: Shotgun.  
 Location/Qualifiers  
 1..12  
 /organism="Trypanosoma cruzi"  
 /mol\_type="genomic DNA"  
 /strain="CL-Brener"  
 /db\_xref="taxon:5693"  
 /clone="G35A7"  
 /cell\_type="epimastigote"  
 /clone\_lib="Trypanosoma cruzi random genomic library"  
 /note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range

was gel purified and cloned into the dephosphorylated  
HincII site of the vector"

## ALIGNMENT SCORES:

Pred. No.: 2.51e+06 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AQ903019 (1-12)

QY 58 G|U|L|U|L|U| 60  
| | | | | | | |  
Db 1 GAAC|TTT|TA 9

RESULT 86 BH127723 12 bp DNA linear GSS 23-JUL-2001  
LOCUS BH127723  
DEFINITION G-1621.r Maize Random Small-insert Genomic Library Zea mays genomic  
clone G-1621 both, genomic survey sequence.  
ACCESSION BH127723  
VERSION BH127723.1 GI:14995555  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 12)  
AUTHORS Meyers,B.C., Tingey,S.V. and Morgante,M.  
TITLE Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome

JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
MEDLINE 21475670  
PubMed 11591643  
COMMENT Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M3reverse  
Class: Shotgun.

FEATURES  
source Location/Qualifiers  
1..12  
/organism="Zea mays"  
/mol\_type="Genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="G-1621"  
/sex="hermaphrodite"  
/tissue\_type="leaf"  
/cell\_type="Young leaf"  
/dev\_stage="seedling"  
/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: PCR-Script; Total genomic DNA was  
nebulized; ends were polished with Pfu polymerase and the  
fragments cloned into PCR-Script."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.51e+06 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0

DB: 28 Gaps: 0  
US-09-966-880A-8 (1-198) x BH127723 (1-12)

QY 36 A|T|G|A|P|S|E|r 38  
| | | | | | | |  
Db 1 CGGAG|G|G|C 9

RESULT 87 BH129328 12 bp DNA linear GSS 23-JUL-2001  
LOCUS BH129328  
DEFINITION G-5a10.f Maize Random Small-insert Genomic Library Zea mays genomic  
clone G-5a10 both, genomic survey sequence.  
ACCESSION BH129328  
VERSION BH129328.1 GI:14997569  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 12)  
AUTHORS Meyers,B.C., Tingey,S.V. and Morgante,M.  
TITLE Abundance, distribution and transcriptional activity of repetitive  
elements in the maize genome  
JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
MEDLINE 21475670  
PubMed 11591643  
COMMENT Contact: Morgante M  
Suite 200  
Dupont Genomics  
PO Box 6104, Newark, DE 19714-6104, USA  
Tel: 302 631 2638  
Fax: 302 631 2607  
Email: Michele.morgante@usa.dupont.com  
Sequences were trimmed to include only high quality bases; forward  
and reverse reads were assembled when significant overlaps were  
detected.  
Seq primer: M3univ  
Class: Shotgun.

FEATURES  
source Location/Qualifiers  
1..12  
/organism="Zea mays"  
/mol\_type="Genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="G-5a10"  
/sex="hermaphrodite"  
/tissue\_type="leaf"  
/cell\_type="Young leaf"  
/dev\_stage="seedling"  
/clone\_lib="Maize Random Small-insert Genomic Library"  
/note="Vector: PCR-Script; Total genomic DNA was  
nebulized; ends were polished with Pfu polymerase and the  
fragments cloned into PCR-Script."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.51e+06 Length: 12  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x BH129328 (1-12)

QY 123 P|G|G|U|G|U|G| 125  
| | | | | | | |  
Db 1 CCGGAG|G|G|C 9

RESULT 88 CG677120/c

LOCUS CG677120 12 bp DNA linear GSS 03-OCT-2003  
 DEFINITION tme0875 tnf Aegilops tauschii genomic clone tnf1C15, genomic  
 survey sequence.  
 ACCESSION CG677120  
 VERSION CG677120.1 GI:37506044  
 KEYWORDS GSS.  
 SOURCE Aegilops tauschii  
 ORGANISM Aegilops tauschii  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Aegilops.  
 1 (bases 1 to 12)  
 Li, W., Zhang, P., Fellera, J., Friebe, B. and Gill, B.S.  
 Sequence composition, organization and evolution of a basic  
 Triticeae genome of the grass family  
 Unpublished (2003)  
 JOURNAL Contact: Li, W  
 Dr. Bikram S. Gill's Lab  
 Wheat Genetics Resource Center, Kansas State University  
 4024 Throckmorton, Manhattan, KS 66506-5502, USA  
 Tel: 785-532-1108  
 Fax: 785-532-5692  
 Email: wli@ksu.edu  
 Seq primer: 17  
 Class: sheared ends.  
 FEATURES  
 source 1..12  
 location/Qualifiers  
 /organism="Aegilops tauschii"  
 /mol\_type="genomic DNA"  
 /strain="AL 8/78"  
 /db\_xref="taxon:37682"  
 /clone="tm17C15"  
 /tissue\_type="leaves"  
 /dev\_stage="shoot"  
 /lab\_host="E. coli strain DH5alpha"  
 /clone\_lib="tmf"  
 /note="Vector: PCR 4Bunt-TOP, 0.8-1.2 kb methylation  
 filtered genomic DNA library"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.51e+06 Length: 12  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 Gaps: 0  
 DB: 29  
 US-09-966-880a-8 (1-198) x CG677120 (1-12)  
 QY 2 ASPSerLeu 4  
 |||||  
 Db 9 GATTCGCTTA 1  
 RESULT 89  
 HSM007977/c  
 ID HSM007977 standard; mRNA; EST; 13 BP.  
 XX  
 AC AL043127;  
 XX  
 SV AL043127.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434D223\_r1 (from clone DKFZp434D223)  
 XX  
 KW EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Euteleostomi; Primates; Catarrhini; Homidae; Homo.  
 XX

RN [1]  
 RP Blum H., Baueraachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RA  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferseitz 18a D-82152 Martinstried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No BL sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 XX  
 FH Key location/Qualifiers  
 FT source 1..13  
 FT /db\_xref="taxon:9606"  
 FT /mol\_type="mRNA"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp434D223"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 FT  
 XX  
 SQ Sequence 13 BP; 2 A; 4 C; 4 G; 3 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2.73e+06 Length: 13  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 Gaps: 0  
 DB: 2  
 US-09-966-880a-8 (1-198) x HSM007977 (1-13)  
 QY 193 PheArgThr 195  
 |||||  
 Db 11 TTCGGAGCC 3  
 RESULT 90  
 AA918967 13 bp mRNA linear EST 10-JUN-1998  
 LOCUS AA918967  
 DEFINITION c182g05.s1 NCI CGAP Kids Homo sapiens cDNA clone IMAGE:1536152 3'  
 similar to TR:Q65566 Q65566; contains element PTR7 repetitive  
 element; mRNA sequence.  
 ACCESSION AA918967  
 VERSION AA918967.1 GI:3058857  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euteleostomi; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 13)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILM at:  
 www-bio.liml.gov/btrp/image/image.html  
 Trace considered overall poor quality  
 Insert length: 1058 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

# FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1536152"
/issue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_1lb="NCI_CGAP_Kids"
/notes="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGAGAGATTGCGCGCGGATTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
```

# ORIGIN

## Alignment Scores:

```
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0
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US-09-966-880A-8 (1-198) x AA918967 (1-13)

QY 90 CysAlaArg 92  
|||||  
Db 3 TGTGCGCGT 11

RESULT 91  
A1744941/c 13 bp mRNA linear EST 21-JUN-1999  
LOCUS t171e03.x1 NCI\_CGAP\_Ov23 Homo sapiens cDNA clone IMAGE:2218588 3'  
DEFINITION similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST; mRNA sequence.  
ACCESSION A1744941  
VERSION A1744941.1 GI:5113229  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

COMMENT  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 13)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNM at:  
www-bio.llnl.gov/bbrp/image/image.html

# JOURNAL

## COMMENT

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

# FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2218588"
```

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/issue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_1lb="NCI_CGAP_Ov23"
/notes="Organ: ovary; Vector: pCMV-SPORT6, Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.35 kb. Tumor types include: mixed  
Mullerian tumor, papillary serous, clear cell, spindle  
cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"
```

# ORIGIN

## Alignment Scores:

```
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0
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US-09-966-880A-8 (1-198) x A1744941 (1-13)

QY 59 LeuLeuPhe 61  
|||||  
Db 11 TTGTGCTT 3

RESULT 92  
BG926067 13 bp mRNA linear EST 06-NOV-2001  
LOCUS HNC23-1-B8.HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
DEFINITION sequence.  
ACCESSION BG926067.1 GI:14320590  
VERSION BG926067.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

# REFERENCE

1 (bases 1 to 13)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathre,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Cowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries  
Osteoarthritis. Cartil. 9 (7), 641-653 (2001)

# JOURNAL

## COMMENT

CONTACT: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsk.com  
Seq primer: 17.  
Location/Qualifiers

# FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="Cartilage"
/lab_host="E.coli DH10 B"
/clone_1lb="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;  
Directional"
```

# ORIGIN

## Alignment Scores:

```
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
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DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG926067 (1-13)

QY 181 Leuphelen 183  
|||||  
1 CTCCTTCTG 9

RESULT 93  
BG927437 13 bp mRNA linear EST 06-NOV-2001  
LOCUS HNC1.1-17.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
DEFINITION BG927437  
ACCESSION BG927437  
VERSION BG927437.1 GI:14321960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 13)  
Kumar,S., Connor,J.R., Dodde,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651  
PUBMED 11597177  
COMMENT Contact: Sanjay Kumar  
UM2109  
GlasgowKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsf.com  
Seq primer: T7,  
Location/Qualifiers  
1..13  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="cartilage"  
/lab\_host="E.Coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

FEATURES  
source

ORIGIN

Alignment Scores:  
Pred. No.: 2.73e+06 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG927437 (1-13)

QY 60 Leuphelen 62  
|||||  
1 CTCCTTCTG 9

RESULT 94  
BM395292/c 13 bp mRNA linear EST 17-JAN-2002  
LOCUS BM395292  
DEFINITION 50072-2-8-D08.f.2 Chlcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM395292  
VERSION BM395292.1 GI:18195345  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE 1 (bases 1 to 13)  
Turkewitz,A.P., Karter,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
TITLE Contact: Turkewitz AP  
JOURNAL Molecular Genetics and Cell Biology  
COMMENT University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1..13  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"

FEATURES  
source

ORIGIN

Alignment Scores:  
Pred. No.: 2.73e+06 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM395292 (1-13)

QY 72 Proglyarg 74  
|||||  
11 CCAGGGCGT 3

RESULT 95  
BM395672/c 13 bp mRNA linear EST 17-JAN-2002  
LOCUS 5009-0-1-H10.c.1 Chlcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM395672  
VERSION BM395672.1 GI:18195725  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE 1 (bases 1 to 13)  
Turkewitz,A.P., Karter,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
TITLE Contact: Turkewitz AP  
JOURNAL Molecular Genetics and Cell Biology  
COMMENT University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1..13  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"

FEATURES  
source

## ORIGIN

/clone\_1lb="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## Alignment Scores:

Pred. No.: 2.73e+06 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM395672 (1-13)

QY 77 ArgValThr 79

DB 10 CGCGTGACC 2

## RESULT 96

BQ586028/c

LOCUS

DEFINITION BQ586028 13 bp mRNA linear EST 06-DEC-2002  
E012394-024-013-F21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
024-013-F21 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaam@mpiz-koeln.mpg.de  
Insert length: 13 Std Error: 0.00  
Plate: 13 row: F column: 21  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. 13  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultiivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:186838"  
/db\_xref="taxon:161934"  
/clone="024-013-F21"  
/issue\_type="leaf"  
/lab\_host="EMDH108"  
/clone\_1lb="MP12-ADIS-024-leaf"  
/note="Vector: PCWVSFOR16; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulze@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SaliI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

## FEATURES

source

/clone\_1lb="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:

Pred. No.: 2.73e+06 Length: 13  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586028 (1-13)

QY 172 LeuSerArg 174

DB 10 TTATGACGA 2

## RESULT 97

BQ589768

LOCUS

DEFINITION BQ589768 13 bp mRNA linear EST 06-DEC-2002  
E012680-024-020-D03-SP6 MP12-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-020-D03 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaam@mpiz-koeln.mpg.de  
Insert length: 13 Std Error: 0.00  
Plate: 20 row: D column: 03  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. 13  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultiivar="KWS2320 (double haploid, monogerm breeding  
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/db\_xref="GABI:190356"  
/db\_xref="taxon:161934"  
/clone="024-020-D03"  
/issue\_type="storage root"  
/lab\_host="EMDH108"  
/clone\_1lb="MP12-ADIS-024-storage root"  
/note="Vector: PCWVSFOR16; Site 1: SalI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulze@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-SaliI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

## FEATURES

source

/clone\_1lb="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:

Pred. No.: 2.73e+06 Length: 13

Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ595423 (1-13)

QY 60 Leuphelen 62  
 |||||  
 3 CTCTCTG 11

RESULT 98  
 BQ595423

LOCUS BQ595423 13 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012693-024-022-N20-SP6 MP12-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-022-N20 5-PRIME, mRNA sequence.

ACCESSION BQ595423.1 GI:26125006  
 VERSION BQ595423.1  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 13)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE JOURNAL MEDLINE  
 PUBMED 22362189  
 COMMENT 12472698

CONTACT: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 13 Std Error: 0.00  
 Plate: 22 row: N column: 20  
 Seq primer: SP6, CATACGATTAGTGACACTATAG.

FEATURES  
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 /db\_xref="GABI:191428"  
 /db\_xref="taxon:161934"  
 /clone="024-022-N20"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinfanzlebeher Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-SPRIME-CDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

# ORIGIN

Alignment Scores:  
 Pred. No.: 2.73e+06 Length: 13  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0

DB: 13 Gaps: 0  
 US-09-966-880A-8 (1-198) x BQ595423 (1-13)

QY 167 G1uanser 169  
 |||||  
 1 GAGATTC 9

RESULT 99  
 BQ595471

LOCUS BQ595471 13 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012691-024-022-C18-SP6 MP12-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-022-C18 5-PRIME, mRNA sequence.

ACCESSION BQ595471  
 VERSION BQ595471.1 GI:26125054  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 13)  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE JOURNAL MEDLINE  
 PUBMED 22362189  
 COMMENT 12472698

CONTACT: Weishaar B  
 ADIS DNA core facility at MP12  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 13 Std Error: 0.00  
 Plate: 22 row: C column: 18  
 Seq primer: SP6, CATACGATTAGTGACACTATAG.

FEATURES  
 source Location/Qualifiers  
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 /organism="Beta vulgaris"  
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 /cultiivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:191389"  
 /db\_xref="taxon:161934"  
 /clone="024-022-C18"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinfanzlebeher Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-SPRIME-CDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

# ORIGIN

Alignment Scores:  
 Pred. No.: 2.73e+06 Length: 13  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ595471 (1-13)

```

Qy      175 GlnLeuArg 177
Db      4 CAACTGAGG 12

RESULT 100
LOCUS   CA794347
DEFINITION CA794347 13 bp mRNA linear EST 05-DEC-2002
Theobroma cacao cDNA clone Cac_Bl_1304 5', mRNA sequence.
ACCESSION CA794347
VERSION   CA794347.1 GI:26051423
KEYWORDS  EST.
SOURCE    Theobroma cacao (cacao)
ORGANISM  Theobroma cacao
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eustosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
TITLE     Gene discovery and microarray analysis of cacao (Theobroma cacao
JOURNAL   Planta 216 (2), 255-264 (2002)
MEDLINE   22337596
PUBMED    12447539
COMMENT   Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.affem.com
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..13
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone="Cac_Bl_1304"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_Bl (bean and leaf from Amelonado type
cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

ORIGIN
Alignment Scores:
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA794347 (1-13)

Qy      82 ThrSerTrp 84
Db      2 ACGTCTTGG 10

RESULT 101
LOCUS   CF299938
DEFINITION 13 bp mRNA linear EST 15-AUG-2003
7LEAF--04-C12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-C12, mRNA sequence.
ACCESSION CF299938
VERSION   CF299938.1 GI:33671699
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa

```

```

REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-C12"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Alignment Scores:
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF299938 (1-13)

Qy      113 LeuTyrPhe 115
Db      12 TTTATTTT 4

RESULT 102
LOCUS   CF306112
DEFINITION HDAL--02-L18.g1 OSHDACL-overexpressing transgenic rice lambda phage
cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--02-L18, mRNA
sequence.
ACCESSION CF306112
VERSION   CF306112.1 GI:33677873
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..13

```

```

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1-02-118"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/notes="vector: pBlueScript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

```

## ORIGIN

## Alignment Scores:

Pred. No.:	2.73e+06	Length:	13
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) X CF306112 (1-13)

QY 38 SerAlaThr 40

Db 10 AGTGCACCC 2

## RESULT 103

CF543088 13 bp mRNA linear EST 22-SEP-2003  
 LOCUS 5014680-024-030-P08-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 DEFINITION 024-030-P08 5-PRIME, mRNA sequence.

ACCESSION CF543088

VERSION CF543088

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 13)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wronk,W., Menze,A., O'Brien,J., Lehrach,H.,  
and Radloff,U.TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert length: 13 Std Error: 0.00

Plate: 30 row: P column: 08

Seq primer: SP6.

## FEATURES

```

source
1..13
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:936675"
/db_xref="taxon:161934"
/clone="024-030-P08"
/tissue_type="leaf"
/lab_host="EMDH105"

```

```

/clone_lib="MP1Z-ADIS-024-leaf"
/notes="vector: PCWVS006; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. library provided by KWS
Kleinmannleber Saatzucht AG Rindbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
project granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RBPd/GABI-Primary database: http://gabi.rzpd.de"

```

## ORIGIN

## Alignment Scores:

Pred. No.:	2.73e+06	Length:	13
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) X CF543088 (1-13)

QY 171 ArgLeuSer 173

Db 12 CGCCTCTCA 4

## RESULT 104

CF921303 13 bp mRNA linear EST 05-NOV-2003  
 LOCUS gmrhbw3-07 G12\_1\_084 Soybean root hair subtracted cDNA library  
 DEFINITION gmrhbw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF921303

VERSION CF921303

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 13)

AUTHORS Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

TITLE Expressed sequence tags from soybean root hair subtractive cDNA  
library

JOURNAL Unpublished (2003)

COMMENT Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-4752

Fax: 573-882-0588

Email: stacey@missouri.edu

Single pass sequence

Seq primer: T7

## FEATURES

```

source
1..13
Location/Qualifiers
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmrhbw3"
/notes="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradryrhizobium japonicum for 3 hours."

```

Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0
US-09-966-880A-8	(1-198) x CF921303	(1-13)	

Qy	41	SerpheSer	43
Db	13	TCCTTTCT	5

RESULT	105
BH170808/c	
LOCUS	
DEFINITION	BH170808
ACCESION	SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_003378, genomic survey sequence.
	n1176660

SOURCE ORGANISM	Arabidopsis thaliana (thale cress)
Arabidopsis thaliana	

TITLE	A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL	Arabidopsis Genome
COMMENT	Unpublished (2001)
	Contact: Joseph R. Ecker

STAFF: JOHN CAGNEY.

## CONCLUSIONS

Alignment Scores:	
Pred. No.:	2.73e+06
Score:	3.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	1.52%
DB:	28
Length:	1
Matches:	3
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-966-880A-8 (1-198) X BH170808 (1-13)

QY	129	LeuHisArg	131
Db	13	CTTCACCGC	5

RESULT 106  
HSM003815/c  
ID HSM003815 standard; mRNA; EST; 14 BP  
XX

AC	AL039339;
XX	
SV	AL039339.1

DT	12-MAR-1999 (Rel. 59, Created)
DT	12-MAR-1999 (Rel. 59, Last updated, Version 1)
...	

DE Homo sapiens mRNA; EST DKFZp434F1810\_r1 (from clone DKFZp434F1810)  
XX  
KW EST; expressed sequence tag.

05 Homo sapiens (human)  
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia  
0C Eutheria; Primates; Catarrhini; Hominoidea; Homo.

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.,

RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Oigsen within the cDNA  
CC  
CC Sequencing consortium of the German Genome Project  
CC No SI sequence available  
CC  
CC This clone is available at the RZPD in Berlin  
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14055  
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

50 Sequence 14 BP; 3 A; 4 C; 4 G; 3 T; 0 other;

Alignment Scores:	
Pred. No.:	2.95e+6
Score:	3.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	1.5%
DB:	2
Gaps:	0
Length:	14
Matches:	3
Conservative:	0
Mismatches:	0
Indels:	0

US-09-966-880A-8 (1-198) x HSM003815 (1-14)

Qy 193 pheargThr 195

RESULT	107
HSMM004378/c	
ID	HSMM004378
	standard; mRNA; EST; 14 BP

DT	12-MAR-1999 (Rel. 59, Created)
DT	12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434G2412\_r1 (from clone DKFZp434G2412, ...)

KW EST; expressed sequence tag.

OS Homo sapiens (human

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.  
 XX  
 RN  
 RP 1-14  
 RA Duesterhoeft A., Lauber J., Mewes W., Gaessnerhuber J., Wiemann S.;  
 RT ;  
 RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferstr 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC No st sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 CC  
 XX  
 FH  
 FH Key Location/Qualifiers  
 FT source 1. .14  
 FT /db\_xref="taxon:9606"  
 FT /mol\_type="mRNA"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 FT  
 XX  
 SQ Sequence 14 BP; 2 A; 5 C; 4 G; 3 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880A-8 (1-198) x HSM004378 (1-14)  
 QY 193 PheargThr 195  
 DB 10 TTCGGCACC 2  
 RESULT 108  
 BG924475 14 bp mRNA linear EST 06-NOV-2001  
 LOCUS HNC27-1-D6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 DEFINITION  
 accession BG924475.1 GI:14318998  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 14)  
 Kumer,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE 21482651  
 PUBMED 11597177  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com  
 Seq primer: T7.  
 Location/Qualifiers  
 1. .14  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSport 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880A-8 (1-198) x BG924475 (1-14)  
 QY 111 AlargLeu 113  
 DB 1 GCCGACATC 9  
 RESULT 109  
 BM399228 14 bp mRNA linear EST 17-JAN-2002  
 LOCUS 5009-0-55-Cl2.t.2 Chlloact/Turkewitz cDNA (large fraction)  
 DEFINITION  
 accession BM399228.1 GI:18199281  
 VERSION  
 KEYWORDS  
 EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM  
 Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
 Hymenostomatida; Tetrahymenida; Tetrahymena.  
 1 (bases 1 to 14)  
 Turkewitz,A.P., Karier,K.M., Jahn,C., Orlas,E., Kirk,K.E.,  
 Frankel,J. and Klobutcher,L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
 1. .14  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chlloact/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library  
 preparation can be found in Chlloact and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM5939228 (1-14)

QY 77 ArgvAlThr 79  
 |||||  
 DB 10 CCGGTGACT 2

RESULT 110 14 bp mRNA linear EST 06-DEC-2002  
 BM590387/c  
 LOCUS E012840-024-019-G10-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 DEFINITION CDNA clone 024-019-G10 5-PRIME, mRNA sequence.

ACCESSION BM590387  
 VERSION BM590387.1 GI:26119970  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 14)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.

AUTHORS  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@piz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 19 row: G column: 10  
 Seq primer: SP6: CATGAGTTTAGTGACACTATAG.  
 Location/Qualifiers

## FEATURES

source

1..14  
 /organism="Beta vulgaris"  
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 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
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 /db\_xref="taxon:161934"  
 /clone="024-019-G10"  
 /issue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCAGCGCTCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BeeT project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BM590387 (1-14)

QY 118 AspArgTyr 120  
 |||||

DB 10 GACAGGAAAG 2

RESULT 111 14 bp mRNA linear EST 06-DEC-2002  
 BM590450  
 LOCUS E012839-024-019-A07-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 DEFINITION CDNA clone 024-019-A07 5-PRIME, mRNA sequence.

ACCESSION BM590450  
 VERSION BM590450.1 GI:26120033  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 14)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.

AUTHORS  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@piz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 19 row: A column: 07  
 Seq primer: SP6: CATGAGTTTAGTGACACTATAG.  
 Location/Qualifiers

## FEATURES

source

1..14  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:189667"  
 /db\_xref="taxon:161934"  
 /clone="024-019-A07"  
 /issue\_type="storage root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinfanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCAGCGCTCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BeeT project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BM590450 (1-14)

QY 61 PheLeuArg 63  
 |||||

DB 4 TTCTGAGG 12  
 |||||

RESULT 112  
 BM593541

LOCUS BQ593541 14 bp mRNA linear EST 06-DEC-2002  
 DEFINITION S013408-024-026-P02-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-026-P02 5-PRIME, mRNA sequence.  
 ACCESSION BQ593541  
 VERSION BQ593541.1 GI:26123124  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant U. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 26 row: P column: 02  
 Seq primer: SP6; CATACGATTTCAGTGACACTATAG.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:19314"  
 /db\_xref="taxon:161934"  
 /clone="024-026-P02"  
 /issue\_type="developing root"  
 /lab\_host="EMDH108"  
 /lab\_host="EMDH108"  
 /clone\_11b="MP1Z-ADIS-024-developing root"  
 /note="Vector: PCWVSFOR6; Site\_1: Sall; Site\_2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sall-NotI, primer sites and  
 orientation:  
 SP6-Sall-CCACGCTCCG-5prime-cDNA-polya-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880A-8 (1-198) x BQ593541 (1-14)  
 QY 43 SerLeuasp 45  
 DB 5 TCTCTGCAC 13  
 RESULT 113 14 bp mRNA linear EST 06-DEC-2002  
 LOCUS BQ593808  
 DEFINITION E012763-024-026-007-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-026-007 5-PRIME, mRNA sequence.  
 ACCESSION BQ593808

VERSION BQ593808.1 GI:26123391  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant U. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 26 row: O column: 07  
 Seq primer: SP6; CATACGATTTCAGTGACACTATAG.  
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 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:193044"  
 /db\_xref="taxon:161934"  
 /clone="024-026-007"  
 /issue\_type="developing root"  
 /lab\_host="EMDH108"  
 /lab\_host="EMDH108"  
 /clone\_11b="MP1Z-ADIS-024-developing root"  
 /note="Vector: PCWVSFOR6; Site\_1: Sall; Site\_2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sall-NotI, primer sites and  
 orientation:  
 SP6-Sall-CCACGCTCCG-5prime-cDNA-polya-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880A-8 (1-198) x BQ593808 (1-14)  
 QY 42 PheSerLeu 44  
 DB 6 TTCTCCCTC 14  
 RESULT 114 14 bp mRNA linear EST 05-DEC-2002  
 LOCUS CA798290  
 DEFINITION Cac Bl\_611 Cac Bl (Bean and leaf from Ameljonardo type Cacao)  
 Theobroma cacao cDNA clone Cac\_Bl\_611 5', mRNA sequence.  
 ACCESSION CA798290  
 VERSION CA798290.1 GI:26055376  
 KEYWORDS EST.  
 SOURCE Theobroma cacao (cacao)  
 ORGANISM Theobroma cacao

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.

1 (bases 1 to 14)

REFERENCE  
AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.  
TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties  
JOURNAL Planta 216 (2), 255-264 (2002)  
MEDLINE 2237596  
PubMed 12447539

COMMENT  
Contact: Jones, Paul  
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG  
Tel: +44 1664 416644  
Email: Paul.Jones@eu.affem.com  
Seq primer: T3.

FEATURES  
source  
Location/Qualifiers

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/organism="Theobroma cacao"  
/mol\_type="mRNA"  
/strain="Amelonado type"  
/db\_xref="taxon:3641"  
/clone="Cac BL 611"  
/tissue\_type="Mature leaf and mature bean"  
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/lab\_host="Xl-1 Blue MRP"  
/clone\_1ib="Cac BL (Bean and leaf from Amelonado type Cacao)"  
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."

# ORIGIN

Alignment Scores:  
Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA798290 (1-14)

Qy 112 ArgLeuTyr 114  
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Db 4 CGCCTATAC 12

RESULT 115  
CA853334/c 14 bp mRNA linear EST 01-AUG-2003  
LOCUS B07A06.5, mRNA sequence.  
DEFINITION B07A06.5, mRNA sequence.  
ACCESSION CA853334  
VERSION CA853334.1 GI:33390127  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max

REFERENCE  
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.  
TITLE Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
Unpublished (2002)  
Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg.006, Km 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA

Tel: 301 504 5750  
Fax: 301 504 5728  
Email: alkharouf@ars.usda.gov.  
Location/Qualifiers

1..14  
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/db\_xref="taxon:3647"  
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/tissue\_type="Roots"  
/dev\_stage="Seedlings"  
/clone\_1ib="CDNA Peking library 12hr SCN3"  
/note="Vector: pBluescript SK-; CDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

# ORIGIN

Alignment Scores:  
Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA853334 (1-14)

Qy 179 IleLeuLeu 181  
|||||  
Db 14 ATCTTGCTC 6

RESULT 116  
CF278327 14 bp mRNA linear EST 14-AUG-2003  
LOCUS 14FTL--04-D06.b1 Rice etiolated leaf plasmid CDNA library (14FTL)  
DEFINITION Oryza sativa CDNA clone 14FTL--04-D06, mRNA sequence.  
ACCESSION CF278327  
VERSION CF278327.1 GI:33655713  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1..14  
/organism="Oryza sativa"  
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/db\_xref="taxon:4530"  
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/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_1ib="Rice etiolated leaf plasmid CDNA library (14FTL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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ORIGIN
Alignment Scores:
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  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 1.52%      Indels: 0
  DB: 14              Gaps: 0

US-09-966-880A-8 (1-198) x CF278327 (1-14)

Oy  34  Lythrag 36
    |||||
Db  12  AAGGAGAGA 4

RESULT 117
CF300543      14 bp  mRNA  linear  EST 15-AUG-2003
LOCUS         7LEAF--05-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION    sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION     CF300543
VERSION       CF300543.1  GI:33672304
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
TITLE         Unpublished (2003)
JOURNAL
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
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    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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    with oligoribonucleotides and then used as templates for
    RT-PCR."
ORIGIN
Alignment Scores:
  2.95e+06      Length: 14
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  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 1.52%      Indels: 0
  DB: 14              Gaps: 0

US-09-966-880A-8 (1-198) x CF300543 (1-14)

Oy  107  Argleph 109
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Db  2  AGAATTTT 10

RESULT 118
CF300543/c

```

```

LOCUS         CF300543      14 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION    7LEAF--05-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION     CF300543
VERSION       CF300543.1  GI:33672304
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
TITLE         Unpublished (2003)
JOURNAL
COMMENT       Contact: Nahm B.H.
              Genomics and Genetics Institute, Greengene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
FEATURES
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    /rissue_type="leaf"
    /dev_stage="7 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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    RT-PCR."
ORIGIN
Alignment Scores:
  2.95e+06      Length: 14
  Score: 3.00    Matches: 3
  Percent Similarity: 100.00%  Conservative: 0
  Best Local Similarity: 100.00%  Mismatches: 0
  Query Match: 1.52%      Indels: 0
  DB: 14              Gaps: 0

US-09-966-880A-8 (1-198) x CF300543 (1-14)

Oy  15  Phelysaen 17
    |||||
Db  13  TTTAAANT 5

RESULT 119
CF306911      14 bp  mRNA  linear  EST 15-AUG-2003
LOCUS         HDAL--05-D06.g1 OshDACL-overexpressing transgenic rice lambda phage
              cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--05-D06, mRNA
              sequence.
ACCESSION     CF306911
VERSION       CF306911.1  GI:33678672
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE     1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
TITLE         Unpublished (2003)
JOURNAL
COMMENT       Contact: Nahm B.H.

```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1. 14  
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/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF307189 (1-14)

Ory 194 ArgThrLeu 196

Db 6 AGGACTCTT 14

## RESULT 120

CF307189/c 14 bp mRNA linear EST 15-AUG-2003  
LOCUS HDAL--05-P24.g1 OSHDA1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--05-P24, mRNA  
sequence.

ACCESSION CF307189 GI:33678950

VERSION CF307189.1 GI:33678950  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Bhakryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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## FEATURES

source

Location/Qualifiers  
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## ORIGIN

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Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF307189 (1-14)

Ory 38 SerIaThr 40

Db 10 AGTGCACCC 2

## RESULT 121

CF307495/c 14 bp mRNA linear EST 15-AUG-2003  
LOCUS HDAL--06-N23.g1 OSHDA1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--06-N23, mRNA  
sequence.

ACCESSION CF307495 GI:33679256  
VERSION CF307495.1 GI:33679256  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Bhakryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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/organism="Oryza sativa"  
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/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## FEATURES

source

Location/Qualifiers  
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/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

Alignment Scores:  
Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3

Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 1.52%  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF328966 (1-14)

QY 38 SerAlaThr 40  
 10 AGTGCACC 2

RESULT 122  
 CF328966 14 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--04-B19, mRNA sequence.  
 ACCESSION CF328966 GI:33806172  
 VERSION CF328966.1  
 KEYWORDS Oryza sativa  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
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 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF328966 (1-14)

QY 10 LysPheLeu 12  
 2 AAATTTTA 10

RESULT 123  
 CF328966 14 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--04-B19, mRNA sequence.  
 ACCESSION CF328966  
 VERSION CF328966.1 GI:33806172

KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..14  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="NACL--04-B19"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2.95e+06 Length: 14  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF328966 (1-14)

QY 15 PheLysAsn 17  
 12 TTTAAAT 4

RESULT 124  
 CF921312 14 bp mRNA linear EST 05-NOV-2003  
 LOCUS gmrHW3-07.H10.1.066 Soybean root hair subtracted cDNA library  
 gmrHW3 Glycine max cDNA, mRNA sequence.  
 ACCESSION CF921312  
 VERSION CF921312.1 GI:38192106  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 1 (bases 1 to 14)  
 Scheffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.  
 Expressed sequence tags from soybean root hair subtractive cDNA  
 library  
 Unpublished (2003)  
 Contact: Gary Stacey  
 University of Missouri  
 108 Waters Hall, Columbia, MO 65211, USA  
 Tel: 573-884-4752  
 Fax: 573-882-0588  
 Email: stacey@missouri.edu

Single pass sequence  
Seq primer: T7FEATURES  
Location/Qualifiers

## Source

1. 14  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Williams 82"  
/db\_xref="taxon:3847"  
/tissue\_type="root hairs"  
/clone\_lib="Soybean root hair subtracted cDNA library  
gmhRwv3"  
/note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones  
generated from soybean root hair tissue treated with  
Bradyrhizobium japonicum for 3 hours."

## ORIGIN

## Alignment Scores:

Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF921312 (1-14)

QY 191 AspAlaphe 193

Db 3 GATGCTTC 11

## RESULT 125

BH169716 14 bp DNA linear GSS 03-OCT-2001  
LOCUS BH169716 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_001788, genomic survey sequence.

ACCESSION BH169716  
VERSION BH169716.1 GI:15905091  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 14)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shim,P., Zimmerman,J. and Ecker,U.R.

REFERENCE  
AUTHORS A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome

TITLE  
JOURNAL Contact: Joseph R. Ecker  
COMMENT Unpublished (2001)  
The Salk Institute Genomic Analysis Laboratory (SIGAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

FEATURES  
Source This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1. 14  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_001788"  
/note="Arabidopsis thaliana TDNA insertion lines"  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can

be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)

## ORIGIN

Alignment Scores:  
Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x BH169716 (1-14)

QY 72 ProGlyArg 74

Db 6 CCGGCGCCGT 14

## RESULT 126

BH169716 14 bp DNA linear GSS 03-OCT-2001  
LOCUS BH169716 Arabidopsis thaliana TDNA insertion lines Arabidopsis  
thaliana genomic clone SALK\_001788, genomic survey sequence.

ACCESSION BH169716  
VERSION BH169716.1 GI:15905091  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 14)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,  
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,  
Shim,P., Zimmerman,J. and Ecker,U.R.

REFERENCE  
AUTHORS A Sequence-Indexed Library of Insertion Mutations in the  
Arabidopsis Genome

TITLE  
JOURNAL Contact: Joseph R. Ecker  
COMMENT Unpublished (2001)  
The Salk Institute Genomic Analysis Laboratory (SIGAL)  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

FEATURES  
Source This is single pass sequence recovered from the left border of  
TDNA.  
Class: TDNA tagged.  
Location/Qualifiers  
1. 14  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone\_lib="SALK\_001788"  
/note="Arabidopsis thaliana TDNA insertion lines"  
each of which contains one or more TDNA insertion  
elements. The resultant fragment for each line was  
directly sequenced to determine the genomic sequence at  
the site of insertion. Details of the protocols used can  
be found at [http://signal.salk.edu/cdna\\_protocols.html](http://signal.salk.edu/cdna_protocols.html)

## ORIGIN

Alignment Scores:  
Pred. No.: 2.95e+06 Length: 14  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x BH169716 (1-14)

```

QY      110 ThrAlaArg 112
DB      14 ACGGCCCG 6

RESULT 127
HSM003885/c
ID      HSM003885 standard; mRNA; EST; 15 BP.
XX
XX
XX      AL039409;
XX
XX      AL039409.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434L1010_r1 (from clone DKFZp434L1010)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OS
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX      [1]
XX      1-15
XX      RP
XX      Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      RL
XX      MIPS, Am Klopferseitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX      CC sequencing consortium of the German Genome Project
XX      CC s1 sequence also available
XX      CC This clone is available at the RZPD in Berlin
XX      CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH
XX      FT      source      1..15
XX      FT      /db_xref="taxon:9606"
XX      FT      /mol_type="mRNA"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFZp434L1010"
XX      FT      /clone_1b="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /tissue_type="testis"
XX
SQ      Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 other;
XX
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             2            Gaps:        0

US-09-966-880a-8 (1-198) x HSM003885 (1-15)
QY      193 PheArgThr 195
DB      14 TTCGGAGC 6

RESULT 128
HSM007985/c
ID      HSM007985 standard; mRNA; EST; 15 BP.
XX
XX
XX      AL043135;
XX
XX      AL043135.1
XX

```

```

DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434D0823_r1 (from clone DKFZp434D0823)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OS
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX      [1]
XX      1-15
XX      RP
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      RL
XX      MIPS, Am Klopferseitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMT within the CDNA
XX      CC sequencing consortium of the German Genome Project
XX      CC No s1 sequence available
XX      CC This clone is available at the RZPD in Berlin
XX      CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH
XX      FT      source      1..15
XX      FT      /db_xref="taxon:9606"
XX      FT      /mol_type="mRNA"
XX      FT      /organism="Homo sapiens"
XX      FT      /clone="DKFZp434D0823"
XX      FT      /clone_1b="434 (synonym: htes3). Vector pSport1; host
XX      FT      DH10B; sites NotI + SalI"
XX      FT      /dev_stage="adult"
XX      FT      /tissue_type="testis"
XX
SQ      Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;
XX
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             2            Gaps:        0

US-09-966-880a-8 (1-198) x HSM007985 (1-15)
QY      193 PheArgThr 195
DB      11 TTCGGAGC 3

RESULT 129
HSM008114/c
ID      HSM008114 standard; mRNA; EST; 15 BP.
XX
XX      AL043264;
XX
XX      AL043264.1
XX
XX      AL043264.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434L1223_r1 (from clone DKFZp434L1223)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OS
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX      [1]

```

RP 1-15  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC No s1 sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clonesrzd.de  
 XX  
 FH Key Location/Qualifiers  
 FT 1.15  
 FT /db\_xref="taxon:9606"  
 FT /mol\_type="mRNA"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSport1, host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880a-8 (1-198) x HSM008114 (1-15)  
 QY 193 PheargThr 195  
 DB 11 TTCGGAGCC 3  
 RESULT 130  
 HSM008148/c standard; mRNA; EST; 15 BP.  
 XX  
 AC AL0432298;  
 XX  
 SV AL043298.1  
 XX  
 DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434M2423\_x1 (from clone DKFZp434M2423)  
 XX  
 KM EST; expressed sequence tag.  
 XX  
 OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN 11  
 RP 1-15  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 XX  
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA  
 CC sequencing consortium of the German Genome Project  
 CC No s1 sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clonesrzd.de

XX  
 FH Key Location/Qualifiers  
 FT 1.15  
 FT /db\_xref="taxon:9606"  
 FT /mol\_type="mRNA"  
 FT /organism="Homo sapiens"  
 FT /clone\_lib="434 (synonym: htes3). Vector pSport1, host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"  
 XX  
 SQ Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 2 Gaps: 0  
 US-09-966-880a-8 (1-198) x HSM008148 (1-15)  
 QY 193 PheargThr 195  
 DB 11 TTCGGAGCC 3  
 RESULT 131  
 AL931094 15 bp mRNA linear EST 14-NOV-2002  
 LOCUS AL931094  
 DEFINITION AL931094 NAPI Anopheles gambiae cDNA clone NAPI-P72-D-06-5, mRNA  
 sequence.  
 ACCESSION AL931094  
 VERSION AL931094.1 GI:24973074  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;  
 Anopheles.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Christophides G.K., Blass K., Zdobnov E.M., Carnouch R., Benes V.  
 and Kafatos F.C.  
 TITLE Anopheles gambiae EST, European Molecular Biology Laboratory  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Christophides GK  
 Fotis C. Kafatos laboratory  
 European Molecular Biology Laboratory  
 Meyerhofstrasse 1, 69117 Heidelberg, Germany  
 Tel.: +49 6221 387-440  
 Fax: +49 6221 387-306  
 Email: christophe@embl-heidelberg.de  
 Plate: P72 row: D column: 06.  
 FEATURES  
 source  
 1.15  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="NAPI-P72-D-06-5"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"  
 /note="Vector: pRT73D-Pac (Pharmacia); Site 1: NotI;  
 Site 2: EcoRI; ESTs sequenced from the T7 priming site  
 that reads from the 5' end of cDNA. The NAPI is a  
 directionally cloned and normalized, oligo-T primed cDNA  
 library constructed from a mixture of Anopheles gambiae  
 developmental stages according to: Bonaldo, Lemmon &  
 Soares (1996): Normalization and Subtraction: Two  
 Approaches To Facilitate Gene Discovery, Genome Research  
 6, 791-806."

ORIGIN

Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AL931094 (1-15)

Qy 172 LeuSerArg 174  
 |||||  
 2 CTCAGCAGA 10

RESULT 132  
 AV199466/c  
 LOCUS AV199466 15 bp mRNA linear EST 26-JUL-1999  
 DEFINITION AV199466 Yuiji Kohara unpublished cDNA Caenorhabditis elegans cDNA  
 ACCESSION AV199466  
 VERSION AV199466.1 GI:5583237  
 KEYWORDS EST.  
 SOURCE Caenorhabditis elegans  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE  
 1 (bases 1 to 15)  
 Kohara, Y., Shin-I, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitani, H., Nishigaki, A., Motomashi, T., Zeng, Q., Matanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.  
 Expressed genes in C. elegans  
 Unpublished (1999)

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Yuiji Kohara  
 Genome Biology Lab.  
 National Institute of Genetics  
 Yata 1111, Mishima, Shizuoka 411, Japan  
 Tel: 81-559-81-6854  
 Fax: 81-559-81-6855  
 Email: ykohara@lab.nig.ac.jp.  
 Location/Qualifiers

FEATURES  
 source  
 1. 15  
 /organism="Caenorhabditis elegans"  
 /mol\_type="mRNA"  
 /strain="CB1489 hit-8(e1489)"  
 /db\_xref="taxon:6239"  
 /clone="YK5462"  
 /sex="Thermaphrodite, male"  
 /tissue\_type="whole animal"  
 /dev\_stage="varied"  
 /clone\_lib="Yuiji Kohara unpublished cDNA"

ORIGIN

Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AV199466 (1-15)

Qy 25 ArgGluThr 27  
 |||||  
 11 CGAGAAAC 3

RESULT 133  
 AM059513  
 LOCUS AM059513 15 bp mRNA linear EST 23-AUG-2000  
 DEFINITION AM059513 dnc15.final.cluster.2 (36) DNC15 Homo sapiens cDNA similar to ribosomal protein S17, mRNA sequence.

ACCESSION AM059513  
 VERSION AM059513.1 GI:6651835  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 15)  
 Brenner, S., Williams, S.R., Vernass, E.H., Storck, T., Moon, K., McColium, C., Mao, J.I., Kirchner, J., Eletri, S., Dubridge, R.B., Burcham, T. and Albrecht, G.  
 In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs  
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 10677516  
 Contact: Burcham TS  
 LYNX Therapeutics, Inc.  
 25861 Industrial Blvd., Hayward, CA 94545, USA  
 Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: timbelynxgen.com  
 Sequence obtained from LYNX Therapeutics Megasort technology.  
 Collected from the down-regulated gate. Consensus sequence of 36 sequences in cluster.  
 High quality sequence stop: 15.  
 Location/Qualifiers

FEATURES  
 source  
 1. 15  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
 /cell\_line="THP-1 (THP-202)"  
 /clone\_lib="DNC15"  
 /note="Vector: PCR.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

ORIGIN

Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AM059513 (1-15)

Qy 169 SerValArg 171  
 |||||  
 4 AGTGTACG 12

RESULT 134  
 AM247148  
 LOCUS AM247148 15 bp mRNA linear EST 07-JAN-2000  
 DEFINITION AM247148 2819953.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE12819953 3', mRNA sequence.  
 ACCESSION AM247148  
 VERSION AM247148.1 GI:6590141  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 15)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Other\_ESTs: 2819953.5prime  
 Contact: Robert Strauberg, Ph.D.  
 Email: cga9ba-1@mail.nih.gov  
 Tissue Procurement: DCTD/DTP cDNA library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLV) DNA Sequencing by: Berkeley WGC sequencing Project Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLV at: [www.bio.lnln.gov/bbrp/image/image.html](http://www.bio.lnln.gov/bbrp/image/image.html) Base Calling / Quality Trimming: PHRED from University of Washington Genome Center. Vector PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 13 contiguous PHRED high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

plate: L10W2 row: P column: 2  
High quality sequence stop: 13.  
Location/Qualifiers

PUBMED 11597177  
COMMENT Contact: Sanjay Kumar  
UM2109  
Glasgow/Kline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar@lsgsk.com  
Seq primer: T7.  
Location/Qualifiers

1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819953"  
/issue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NH1\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="cartilage"  
/lab\_host="E. coli DH10 B"  
/clone\_lib="HOA (Human Osteoarthritic Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

ORIGIN

Alignment Scores:

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Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) X AM247148 (1-15)

QY 61 PhelanArg 63  
|||||||  
6 TTTTACGG 14

RESULT 135  
BG900900 15 bp mRNA linear EST 06-NOV-2001  
HOA7-1-A8 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,  
mRNA sequence.  
BG900900  
BG900900.1 GI:1431149  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 15)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathie,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
CONTACT: Sanjay Kumar  
UM2109  
Glasgow/Kline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar@lsgsk.com  
Seq primer: T7.  
Location/Qualifiers

1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/issue\_type="cartilage"  
/lab\_host="E. coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"

ORIGIN /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

## ALIGNMENT SCORES:

Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925415 (1-15)

QY 104 Leuserleu 106

DB 2 CTCCTCTCT 10

## RESULT 137

BG925415/c

LOCUS 15 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC5-1-B1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
ACCESSION BG925415  
VERSION BG925415.1 GI:14319938  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 15)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathie,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteoarthritis cartilage cDNA libraries  
Osteoarthritis Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE  
PUBMED  
COMMENT Contact: Sanjay Kumar  
twn2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@sk.com  
Seq primer: T7.  
Location/Qualifiers  
1. 15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_id="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925415 (1-15)

QY 24 ArgArgGlu 26

DB 12 AGAAGAGAG 4

ORIGIN /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

## ALIGNMENT SCORES:

Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925415 (1-15)

## RESULT 138

BM396203

LOCUS 15 bp mRNA linear EST 17-JAN-2002

DEFINITION 5009-0-18-G08.c.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM396203  
VERSION BM396203.1 GI:18196256  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 15)  
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,  
Frankel,U. and Klobutcher,L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers  
1. 15  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_id="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript SK-; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN  
Alignment Scores:  
Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

QY 83 SerTTPSer 85

DB 6 AGCTGGAGC 14

ORIGIN  
Alignment Scores:  
Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

QY 83 SerTTPSer 85

DB 6 AGCTGGAGC 14

ORIGIN  
Alignment Scores:  
Pred. No.: 3.17e+06 Length: 15 bp mRNA linear EST 17-JAN-2002  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

QY 83 SerTTPSer 85

DB 6 AGCTGGAGC 14

ORIGIN  
Alignment Scores:  
Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.

# FEATURES

Location/Qualifiers

1..15  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
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 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

QY 41 SerPheSer 43

Db 9 AGCTTTTCA 1

RESULT 140

BM398486 15 bp mRNA linear EST 17-JAN-2002  
 LOCUS Tetrahymena thermophila cDNA, mRNA sequence.

DEFINITION BM398486

ACCESSION BM398486.1 GI:18198539

VERSION EST.

KEYWORDS Tetrahymena thermophila

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

AUTHORS Hymenostomatida; Tetrahymena; Tetrahymena.

TITLE 1 (bases 1 to 15)

JOURNAL Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, B., Kirk, K.E.,

COMMENT EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

## FEATURES

Location/Qualifiers

1..15  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
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 /clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398486 (1-15)

QY 111 AlAargLeu 113

Db 7 GCTCGGCTT 15

RESULT 141

BM415446 15 bp mRNA linear EST 28-JAN-2002

LOCUS Op20520 Mixed Stage EST's from Globodera pallida, the potato cyst

DEFINITION nematode Globodera pallida cDNA, mRNA sequence.

ACCESSION BM415446

VERSION BM415446.1 GI:18382117

KEYWORDS EST.

SOURCE Globodera pallida

ORGANISM Globodera pallida

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

AUTHORS Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

TITLE Heer, U., Sosinski, B., Pokrzywa, R.M., Wary, A. and Opperman, C.

JOURNAL Mixed Stage EST's from Globodera pallida, the potato cyst nematode

COMMENT Unpublished (2001)

Contact: Opperman, C

Center for the Biology of Nematode Parasitism

NC State University; IACR-Rothamsted

Campus Box 7616; Raleigh, NC 27695, USA

Tel: 919.515.6639

Fax: 919.515.9500

Email: warthog@ncsu.edu

Gt11-4PCN.F.D05.PCN.4.F.042.ab1.

Location/Qualifiers

1..15  
 /organism="Globodera pallida"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:36090"  
 /clone\_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"  
 /note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM415446 (1-15)

QY 42 PheSerLeu 44

Db 2 TTGAGTCTA 10

RESULT 142

BM584986 15 bp mRNA linear EST 06-DEC-2002

LOCUS BM584986/c

DEFINITION E011826-024-002-K24-SP6 MP12-ADIS-024-inflorescence Beta vulgaris

ACCESSION BM584986

VERSION BM584986.1 GI:26114563

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
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 Plate: 2 row: K column: 24  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
 Location/Qualifiers  
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 /mol\_type="cDNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:181716"  
 /db\_xref="taxon:161934"  
 /clone="024-002-K24"  
 /tissue\_type="inflorescence"  
 /lab\_host="EMDH1.0B"  
 /clone\_lib="MP1Z-ADIS-024-inflorescence"  
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleimanzlebener Saatnucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polYA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-BEET  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880a-8 (1-198) x BQ584986 (1-15)

QY 179 Tleleuenu 181  
 Db 9 ATTCTCTTA 1

RESULT 143  
 BQ588286 15 bp mRNA linear EST 06-DEC-2002  
 LOCUS B012308-024-008-J22-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 DEFINITION 024-008-J22 5-PRIME, mRNA sequence.  
 ACCESSION BQ588286  
 VERSION BQ588286.1 GI:26117869  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
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 Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
 Location/Qualifiers  
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 line)"  
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 /clone="024-008-J22"  
 /tissue\_type="leaf"  
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 /clone\_lib="MP1Z-ADIS-024-leaf"  
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleimanzlebener Saatnucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGCGTCCG-5prime-cDNA-polYA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-BEET  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0  
 US-09-966-880a-8 (1-198) x BQ588286 (1-15)

QY 36 ArgAspSer 38  
 Db 1 CGTCTTCC 9

RESULT 144  
 BQ589356 15 bp mRNA linear EST 06-DEC-2002  
 LOCUS B014008-024-015-K22-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 DEFINITION cDNA clone 024-015-K22 5-PRIME, mRNA sequence.  
 ACCESSION BQ589356  
 VERSION BQ589356.1 GI:26118939  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189

## PUBMED 12472698

COMMENT Contact: Weishaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 15 row: K column: 22  
Seq primer: SP6; CATACGATTAGCTGACACTATAG.  
Location/Qualifiers

## FEATURES

source

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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
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/db_xref="GABI:187717"
/db_xref="taxon:161934"
/clone="024-015-K22"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
```

## ORIGIN

## Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ589356 (1-15)

QY 172 leuserArg 174

DB 2 TTATCAAGA 10

RESULT 145 15 bp mRNA linear EST 06-DEC-2002  
BQ591870/c  
LOCUS E012551-024-016-M20-SP6 MPiZ-ADIS-024-storage root Beta vulgaris

DEFINITION cDNA clone 024-016-M20 5-PRIME, mRNA sequence.  
ACCESSION BQ591870  
VERSION BQ591870.1 GI:26121453  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research

## FEATURES

source

Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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Plate: 16 row: M column: 20  
Seq primer: SP6; CATACGATTAGCTGACACTATAG.  
Location/Qualifiers

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/notes="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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## ORIGIN

## Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
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Percent Similarity: 100.00% Conservative: 0  
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Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591870 (1-15)

QY 131 ArgAlagly 133

DB 9 CGCGCTGGG 1

RESULT 146 15 bp mRNA linear EST 06-DEC-2002  
BQ595631/c  
LOCUS E012693-024-022-B04-SP6 MPiZ-ADIS-024-developing root Beta vulgaris

DEFINITION cDNA clone 024-022-B04 5-PRIME, mRNA sequence.  
ACCESSION BQ595631  
VERSION BQ595631.1 GI:26125214  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weishaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
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 /lab\_host="BMDH10B"  
 /clone\_lib="MP12-ADIS-024-developing root"  
 /note="Vector: PCWVSORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleimanziebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kms.de; cloning site SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence substation managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
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 DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ595631 (1-15)

QY 22 LysGlyArg 24  
 |||||  
 13 AAGGACGA 5

RESULT 147  
 CA796369 15 bp mRNA linear EST 05-DEC-2002  
 LOCUS CAC.BL.3383 CAC.BL. (Bean and leaf from Amelionardo type Cacao)  
 DEFINITION Theobroma cacao cDNA clone CAC.BL.3383 5', mRNA sequence.  
 ACCSSION CA796369 GI:26053445  
 VERSION CA796369.1 GI:26053445  
 KEYWORDS EST.  
 SOURCE Theobroma cacao (cacao)  
 ORGANISM Theobroma cacao

REFERENCE  
 1 (bases 1 to 15)  
 Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.  
 Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties  
 Plantia 216 (2), 255-264 (2002)

JOURNAL MEDLINE  
 22337596  
 PUBMED 12447539  
 COMMENT Contact: Jones, Paul  
 Masterfoods  
 3d Dundee Road, Slough, Berkshire, UK, SL1 4UG  
 Tel: +44 1664 416644  
 Email: Paul.jones@eu.affem.com  
 Seq primer: T3:  
 Location/Qualifiers  
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 /strain="Amelionardo type"

FEATURES  
 Source

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA796369 (1-15)

QY 157 ArgThrPhe 159  
 |||||  
 5 AGGACCTT 13

## RESULT 148

CP303956 15 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF1--03-K24 g1 ABF3-overexpressing transgenic rice lambda phage  
 DEFINITION cDNA library (ABF1) Oryza sativa cDNA clone ABF1--03-K24, mRNA sequence.  
 ACCSSION CP303956  
 VERSION CP303956.1 GI:33675717  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE  
 1 (bases 1 to 15)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /clone="ABF1--03-K24"  
 /issue\_type="leaf"  
 /dev stage="14 days after germination"  
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 /clone\_lib="ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)"  
 /note="Vector: plusscript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

FEATURES  
 source

ORIGIN  
 Alignment Scores:  
 1..15  
 /organism="Theobroma cacao"  
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Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF315668 (1-15)  
 QY 124 GluGlyLeu 126  
 DB 5 GAGCGATT 13  
 RESULT 149  
 CF315668 15 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD--04-K19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION  
 ACCESSION CF315668  
 VERSION CF315668.1 GI:33687429  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 15)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
 location/Qualifiers  
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 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
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 /note="Vector: pCR4-TOPO, Site\_1: EcoRI; Callus was  
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 derived from rice Histone Deacetylase overexpression  
 line."  
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 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF315668 (1-15)  
 QY 86 ProCyStyr 88  
 DB 5 CCTGTATT 13  
 RESULT 150  
 CF316846

LOCUS CF316846 15 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--06-F02.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa cDNA clone HD--06-F02, mRNA sequence.  
 ACCESSION CF316846  
 VERSION CF316846.1 GI:33688607  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 15)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.  
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 derived from rice Histone Deacetylase overexpression  
 line."  
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 Alignment Scores:  
 Pred. No.: 3.17e+06 Length: 15  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF316846 (1-15)  
 QY 49 LeuArgaen 51  
 DB 3 CTACTTAA 11  
 RESULT 151  
 CF317855 15 bp mRNA linear EST 15-AUG-2003  
 LOCUS HD--07-L05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa cDNA clone HD--07-L05, mRNA sequence.  
 ACCESSION CF317855  
 VERSION CF317855.1 GI:33689616  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 15)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
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/lab\_host="E.coli DH10B"  
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CDNA library (HD)"  
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF317855 (1-15)

Ory 59 LeuLeuPhe 61  
|||||  
Db 14 TTATTATTC 6

## RESULT 152

LOCUS CF324208 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION HDN--05-018-g1 OSHDA1-overexpressing transgenic rice lambda phage  
CDNA library II (HDN) Oryza sativa CDNA clone HDN--05-018, mRNA  
sequence.

ACCESSION CF324208  
VERSION CF324208.1 GI:33796681  
KEYWORDS EST.  
SOURCE Oryza sativa

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
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## ORIGIN

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5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## Alignment Scores:

Pred. No.: 3.17e+06 Length: 15  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF324208 (1-15)

Ory 142 LysAspTyr 144  
|||||  
Db 5 AAGATTAC 13

## RESULT 153

LOCUS CF324208/C 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION HDN--05-018-g1 OSHDA1-overexpressing transgenic rice lambda phage  
CDNA library II (HDN) Oryza sativa CDNA clone HDN--05-018, mRNA  
sequence.

ACCESSION CF324208  
VERSION CF324208.1 GI:33796681  
KEYWORDS EST.  
SOURCE Oryza sativa

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
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/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
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/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

## Alignment Scores:

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Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF340248 (1-15)

QY 100 Glyaspro 102
DB 14 GATATCCT 6

RESULT 154 CF340244 15 bp mRNA linear EST 18-AUG-2003
LOCUS RCL1--07-G18.g1 Regenerated callus lambda phage CDNA library (RCL1)
DEFINITION Oryza sativa CDNA clone RCL1--07-G18, mRNA sequence.
ACCESSION CF340244
VERSION CF340244.1 GI:33828846
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehretaceae; Oryzaceae; Oryza.
1 (bases 1 to 15)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahn B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel.: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnah@gbio.com, bhnahmbio.myongji.ac.kr.
FEATURES
Source location/Qualifiers
1..15
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ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF340244 (1-15)

QY 165 Leuhisglu 167
DB 15 CTTCATGAG 7

RESULT 155 CF543306/c

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```

LOCUS CF543306 15 bp mRNA linear EST 22-SEP-2003
DEFINITION S014668-024-029-F24-SP6 MP12-ADIS-024-leaf Beta vulgaris CDNA clone
ACCESSION 024-029-F24 5-PRIME, mRNA sequence.
CF543306
VERSION CF543306.1 GI:34691746
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
REFERENCE Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
AUTHORS Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
and Radefeld,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
JOURNAL fingerprinting allows access to 25 000 potential sugar beet genes
MEDLINE Plant J. 32 (5), 845-857 (2002)
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpl-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Place: 29 row: F column: 24
Seq primer: SP6.
FEATURES
Source location/Qualifiers
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936441"
/db_xref="taxon:161934"
/clone="024-029-F24"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; CDNA library from sugar beet, library provided by KWS Kleimanzeleber Saatnucht AG Binbeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACCGCTCCG-5prime-CDNA-polyA-CC-NotI-T7; Note: sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF543306 (1-15)

QY 193 Pheargthr 195
DB 15 TTTCGACG 7

RESULT 156 CF543404 15 bp mRNA linear EST 22-SEP-2003
LOCUS S014668-024-029-SP6 MP12-ADIS-024-leaf Beta vulgaris CDNA clone
DEFINITION 024-029-D20 5-PRIME, mRNA sequence.
ACCESSION CF543404

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```

VERSION CFS43404.1 GI:34891844
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drumowski,M., Stahl,D., Kruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 29 Row: D Column: 20
Seq primer: SP6.

FEATURES
source
1..15
location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:936359"
/db_xref="taxon:161934"
/clone="024-029-D20"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_idb="MP12-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; site 1: SalI; site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleimenzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CFS43404 (1-15)

QY 193 PheargThr 195
|||||
Db 15 TTTCGACG 7

RESULT 157
R41075 15 bp mRNA linear EST 16-MAY-1995
LOCUS Hk082-f Adult heart, Clontech Homo sapiens cDNA clone K082-f, mRNA
DEFINITION Sequence.
ACCESSION R41075
VERSION R41075.1 GI:798691
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS Wray,M.M.Y., Cheung,H.K.Y., Lam,W.Y., Law,P.T.W., Lo,A.S.Y.,
Lui,V.W.Y., Luk,S.C.W., Tsui,S.K.W., Tung,C.K.C., Yam,N.Y.H.,
Liew,C.C. and Lee,C.Y.
TITLE Gene expression of adult human heart as revealed by random
sequencing of cDNA library
JOURNAL Miami Winter Biotechnol. Symp. Proc. 6, 90 (1995)
COMMENT Contact: Wray Mary M.Y.
Department of Biochemistry
The Chinese University of Hong Kong
Rm 302C, Basic Medical Science Building, The Chinese University of
Hong Kong, Shatin, N.T., Hong Kong.
Tel: 8526096874
Fax: 8526035123
Email: bl33723@vax.csc.cuhk.hk
Seq primer: GGTGGCGACGCTCTGGAGCC.

FEATURES
source
1..15
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="K082-f"
/lab_host="E. coli Y1090"
/clone_idb="Adult heart, Clontech"
/note="Vector: Lambda gfil1, site_1: EcoRI, site_2: EcoRI"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x R41075 (1-15)

QY 170 VALArgLeu 172
|||||
Db 3 GTGCGATTG 11

RESULT 158
HSK001764 standard; mRNA; EST; 16 BP.
ID HSK001764
XX AC AL037434;
XX SV
XX AL037434.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZps5401471_s1 (from clone DKFZps5401471)
XX KW EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX RN [1]
XX RP 1-16
XX RA Bloecher H., Boeher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;
XX MI Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
XX RL MTPS, Km Klopferpitz 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by GBF within the cDNA
XX CC sequencing consortium of the German Genome Project
XX CC No r1 sequence available
XX CC This clone is available at the RZPD in Berlin

```

```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT 1..16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp56401471"
FT /clone_lib="564 (synonym: hfbz2) . Vector pAMP1; host
FT X1-2blue, sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 16 BP; 5 A; 1 C; 0 G; 10 T; 0 other;

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSM001764 (1-16)

Cy 60 Leupheleu 62
Db 3 TTATTTTTA 11

RESULT 159
HSM004270/c standard; mRNA; EST; 16 BP.
ID HSM004270 standard; mRNA; EST; 16 BP.
XX
AC AL039794.1
XX
SV AL039794.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434B1612_x1 (from clone DKFZp434B1612)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX
RN [1]
RP 1-16
RA Dusterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIR3, Am Klopferpitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No. 81 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT 1..16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp434B1612"
FT /clone_lib="434 (synonym: htees) . Vector pSport1; host
FT DH10B; sites NotI + SalI"

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FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 16 BP; 3 A; 4 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSM004270 (1-16)

Cy 193 PheargTnr 195
Db 14 TTCCGAGCC 6

RESULT 160
AA904711/c 16 bp mRNA linear EST 09-JUN-1998
o74d10.81 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1504051 3' similar to TR:015387 015387 34 KDA MOV34 ISOLOGUE.
DEFINITION
AA904711
AA904711 GI:3039834
ACCESSION
AA904711
VERSION
AA904711.1 GI:3039834
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 16)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1732 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cd_name="IMAGE:1504051"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/clone_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NDHL19W, testis NHT, and B-cell
NCT CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0

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DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA939272 (1-16)

QY 154 AsnHISGLU 156

DB 10 AATCATGAG 2

RESULT 161  
AA939272/cLOCUS 16 bp mRNA linear EST 01-MAY-1998  
DEFINITION oq31b06.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587923 3'similar to SW:CA34 HUMAN Q01955 PROCOLLAGEN ALPHA 3(IV) CHAIN  
PRECUSOR, contains OFR.b3 MSRI repetitive element ;, mRNA  
sequence.

ACCESSION AA939272

VERSION AA939272.1 GI:3099185

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnlnl.gov/bbtp/image/image.html

Trace considered overall poor quality  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES

source

1..16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587923"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP GC4"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from 3 pooled

germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified pRT73

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA939272 (1-16)

QY 100 GYAsnPro 102

DB 15 GGAAACCCC 7

RESULT 162  
AA953804/cLOCUS 16 bp mRNA linear EST 07-JUL-1998  
DEFINITION o038c06.s1 NCI CGAP Lm5 Homo sapiens cDNA clone IMAGE:1568458 3'

similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH

7. [2] TR:000280 ;, mRNA sequence.

ACCESSION AA953804

VERSION AA953804.1 GI:3116722

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnlnl.gov/bbtp/image/image.html

FEATURES

source

1..16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1568458"

/tissue\_type="carcinoid"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Lm5"

/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a

modified polylinker; 1st strand cDNA was prepared from

neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated

to Eco RI adaptors (Pharmacia), digested with Not I and

cloned into the Not I and Eco RI sites of the modified

pRT73 vector. Library is normalized. Library was

constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA953804 (1-16)

QY 171 ArgLeuSer 173

DB 9 CGCTTGAGC 1

RESULT 163

AA968729 16 bp mRNA linear EST 27-AUG-1998

LOCUS o09h11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:160157 3'

DEFINITION similar to SW:EPRE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E

/contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AA968729  
 VERSION AA968729.1 GI:3143909  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMD at: [www.bio.1lnl.gov/bbrp/image/image.html](http://www.bio.1lnl.gov/bbrp/image/image.html)

FEATURES  
 source  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1601157"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_1ib="NCI CGAP GC3"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.39e+06 Length: 16  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x AA968729 (1-16)

QY 23 GYATGATG 25  
 |||||  
 Db 5 GCGAGGAGG 13

RESULT 164  
 AA968729/c 16 bp mRNA linear EST 27-AUG-1998  
 LOCUS or59h11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3'  
 DEFINITION similar to SW:RPPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E  
 ;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AA968729  
 VERSION AA968729.1 GI:3143909  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMD at: [www.bio.1lnl.gov/bbrp/image/image.html](http://www.bio.1lnl.gov/bbrp/image/image.html)

FEATURES  
 source  
 1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1601157"  
 /tissue\_type="pooled germ cell tumors"  
 /lab\_host="DH10B"  
 /clone\_1ib="NCI CGAP GC3"  
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.39e+06 Length: 16  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x AA968729 (1-16)

QY 180 LeuLeuPro 182  
 |||||  
 Db 12 CTCCTCCCC 4

RESULT 165  
 A1094839/c 16 bp mRNA linear EST 18-AUG-1998  
 LOCUS q22c08.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'  
 DEFINITION similar to TR:O00599 O00599 CON1. ;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION A1094839  
 VERSION A1094839.1 GI:3433815  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)  
 AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/RTGAP), Tumor Gene Index  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Robert Strausberg, Ph.D.



/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1838200"  
/sex="male"  
/lab\_host="MDH10B"  
/clone\_lib="Soares testis\_NHT"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5', TGTTCACATCTGAATGGAGCGCGCCCAATTTTCTTTTCTTTT 3'] . Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.39e+06 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1208066 (1-16)

Qy 77 ArgValThr 79  
|||||  
2 CGGTCACG 10

Db 2 CGGTCACG 10

RESULT 168 16 bp mRNA linear EST 21-APR-1999  
LOCUS A1603831  
DEFINITION SMOV3MCM27A07SK Onchocerca volvulus molting L3 larva cDNA  
(S196MTM-Ovml3) Onchocerca volvulus cDNA clone SMOV3MCM27A07 5',  
mRNA sequence.

ACCESSION A1603831 GI:4612980

VERSION A1603831.1  
KEYWORDS EST.  
SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Onchocerca.

REFERENCE 1 (bases 1 to 16)  
AUTHORS Williams S.A., Lizotte-Waniewski M., Laney S. and Lustigman S.  
TITLE Genes expressed in molting L3 larvae of Onchocerca volvulus  
JOURNAL Unpublished (1997)  
COMMENT Contact: Steven A. Williams  
Molecular Parasitology  
Smith College Department of Biological Sciences  
Department of Biological Sciences, Clark Science Center, Smith  
College, Northampton, MA, 01063, USA  
Tel: 413653826  
Fax: 413653786  
Email: genome@smith.edu  
Seq primer: Bluescript SK.

FEATURES  
Location/Qualifiers

source

1..16  
/organism="Onchocerca volvulus"  
/mol\_type="mRNA"  
/strain="Kumba, Cameroons"  
/db\_xref="taxon:6282"  
/clone="SMOV3MCM27A07"  
/dev\_stage="molting L3"  
/lab\_host="XLI-Blue WRP"  
/clone\_id="Onchocerca volvulus molting L3 larva cDNA  
(S196MTM-Ovml3)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Filarial nematode parasite of humans. Third-stage

larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (ml3), 2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10<sup>6</sup> independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigman@bc.org)."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.39e+06 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1603831 (1-16)

Qy 48 TyrLeuArg 50  
|||||  
3 TATTTAAG 11

Db 3 TATTTAAG 11

RESULT 169 16 bp mRNA linear EST 07-JAN-2000  
LOCUS A1603831  
DEFINITION 2820844.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820844 3',  
mRNA sequence.

ACCESSION A1603831 GI:6591533

VERSION A1603831.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE Unpublished (1999)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Other ESTs: 2820844.5prime  
Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing  
project clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LIML at:  
www.bio.liml.gov/btrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patchwork.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 15  
contiguous PHRED high quality bases following vector sequence. Very  
low Quality Sequence: trace file contained 16 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

Plate: L1C05 row: E column: 5  
High quality sequence stop: 15.  
Location/Qualifiers

FEATURES  
source

1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db xref="taxon:9606"  
 /clone="IMAGE:2820844"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

## Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM250981 (1-16)

CY 15 Pheylsaa 17

DB 8 TTTAAAC 16

## RESULT 170

AM250981 16 bp mRNA linear EST 07-JAN-2000  
 LOCUS 2822267.3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2822267 3',  
 DEFINITION mRNA sequence.

ACCESSION AM250981

VERSION AM250981.1 GI:6594070

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 16)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2822267.5prime

CONTACT: Robert Strauberg, Ph.D.

Email: cgsbds-remail.nih.gov

Tissue Procurement: DCTD/DBP CDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing

project clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LINL at:

www.bio.lnli.gov/bbtp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 9 contiguous

PHRED high quality bases following vector sequence. Very Low

Quality Sequence: trace file contained 16 contiguous distinct peaks

following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the

beginning of the sequence, this CDNA insert was polyadenylated.

Place: LINC8 row: 9 column: 12

High quality sequence stop: 9.

Location/Qualifiers

1. 16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2822267"

/tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_7"  
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

## Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM250981 (1-16)

CY 118 Aspargly 120

DB 16 GACAGGAAA 8

## RESULT 171

BG897738 16 bp mRNA linear EST 06-NOV-2001  
 LOCUS BG897738  
 DEFINITION HOA17-1-C3 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA,  
 mRNA sequence.

ACCESSION BG897738

VERSION BG897738.1 GI:14307987

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 16)

AUTHORS Kumar, S., Connor, J.R., Dadds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lair, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

MEDLINE 21482651

JOURNAL 11597177

COMMENT Contact: Sanjay Kumar

UM2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar@glk.com

Seq primer: 77.

Location/Qualifiers

1. 16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="cartilage"

/lab\_host="B. coli DH10 B"

/clone\_lib="HOA (Human Osteoarthritic Cartilage)"

/note="vector: pSPORT I; Site\_1: SalI; Site\_2: NotI; Directional"

## ORIGIN

## Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG977738 (1-16)

QY 174 Arginine 176  
 DB 8 AGGAGCTC 16

RESULT 172  
 BG900981

LOCUS H0A52-1-D1.R HOA (Human Osteoarthritic Cartilage) Homo sapiens  
 DEFINITION

ACCESSION BG900981

VERSION BG900981.1 GI:14311230

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Authors Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.

TITLE

Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries

Journal Osteoarthr. Cartil. 9 (7), 641-653 (2001)

Medline 21482651

PubMed 11597177

COMMENT Contact: Sanjay Kumar

ORIGIN

GlaXoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-1@gsk.com

Seq primer: 17.

Location/Qualifiers

source

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="cartilage"

/lab\_host="E.coli DH10 B"

/clone\_id="HOA (Human Osteoarthritic Cartilage)"

/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 12

US-09-966-880A-8 (1-198) x BG900981 (1-16)

QY 41 Serpiner 43

DB 3 AGCTTAGC 11

RESULT 173

BG926060

LOCUS HNC23-1-E1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

DEFINITION

ACCESSION BG926060

VERSION BG926060.1 GI:14320583

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Authors Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.

TITLE

Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries

Journal Osteoarthr. Cartil. 9 (7), 641-653 (2001)

Medline 21482651

PubMed 11597177

COMMENT Contact: Sanjay Kumar

ORIGIN

GlaXoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-1@gsk.com

Seq primer: 17.

Location/Qualifiers

source

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="cartilage"

/lab\_host="E.coli DH10 B"

/clone\_id="HNC (Human Normal Cartilage)"

/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 12

US-09-966-880A-8 (1-198) x BG926060 (1-16)

QY 34 LysArgArg 36

DB 9 AAGAGAGG 1

RESULT 174

BM97104/c

LOCUS 5009-0-28-H09.c.2 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM97104

VERSION BM97104.1 GI:18197157

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 16)

Authors Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortae,E., Kirk,K.E.,  
 Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

CONTACT: Turkewitz AP

MOLECULAR GENETICS AND CELL BIOLOGY

UNIVERSITY OF CHICAGO

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apurkew@midway.uchicago.edu  
Seq primer: T3.

# FEATURES

source  
1.16  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

### Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM397104 (1-16)

OY 77 ArgValThr 79

DB 14 CGCGTGAAG 6

## RESULT 175

BM399406

LOCUS 5009-0-57-D08.t.2 Chlicoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM399406  
VERSION BM399406.1 GI:18199459  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 16)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

source  
1.16  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.39e+06  
Score: 3.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 1.52%  
DB: 12  
Gaps: 0

US-09-966-880A-8 (1-198) x BM401358 (1-16)

OY 77 ArgValThr 79

DB 13 CGCGTGAAG 5

## RESULT 177

BM817126/c

LOCUS 5009-0-9-D08.t.1 Chlicoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM817126  
VERSION BM817126.1 GI:19153140  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 16)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

source  
1.16  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM399406 (1-16)

OY 125 GlyLeuArg 127

DB 8 GGATTAAAG 16

## RESULT 176

BM401358/c

LOCUS 5009-0-9-D08.t.1 Chlicoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM401358  
VERSION BM401358.1 GI:18201411  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 16)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

source  
1.16  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

US-09-966-880A-8 (1-198) x BM401358 (1-16)

## ORIGIN

Alignment Scores:  
Pred. No.: 3.39e+06  
Score: 3.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 1.52%  
DB: 12  
Gaps: 0

## FEATURES

source  
1.16  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

US-09-966-880A-8 (1-198) x BM401358 (1-16)

OY 77 ArgValThr 79

DB 13 CGCGTGAAG 5

## RESULT 177

BM817126/c

LOCUS 5009-0-9-D08.t.1 Chlicoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM817126  
VERSION BM817126.1 GI:19153140  
KEYWORDS EST.  
SOURCE Tetrahymena thermophila  
ORGANISM Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
1 (bases 1 to 16)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apurkew@midway.uchicago.edu  
Seq primer: T3.

## FEATURES

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

TITLE McLaughlin, H., Fredrickson, M.A. and Bohner, H.J.  
Monitoring large-scale changes in transcript abundance in drought-  
and salt-stressed barley  
JOURNAL Unpublished (2002)  
COMMENT Contact: Mark A. Fredrickson  
Plant Biology  
University of Illinois  
1201 W Gregory Dr, Urbana, IL 61801, USA  
Tel: 2172655473  
Email: bohnert@life.uiuc.edu.

## FEATURES

source

```

1..16
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/strain="cv tokak"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HC02D04.T3.ab1"
/tissue_type="Root"
/dev_stage="3 week old"
/clone_lib="HC"
/notes="6 and 10 hour drought stress by placing plants on
moist paper (75% rel. humidity) in light"

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## ORIGIN

Alignment Scores:  
Pred. No.: 3.39e+06 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM817126 (1-16)

QY 133 GLYVALGN 135

Db 11 GGAGTACAA 3

## RESULT 178

BO585399 16 bp mRNA linear EST 06-DEC-2002  
LOCUS S011421-024-001-L05-SP6R MP12-ADIS-024-inflorescence Beta vulgaris  
DEFINITION cDNA clone 024-001-L05-5-PRIME, mRNA sequence.  
ACCESSION BO585399  
VERSION BO585399.1 GI:26114981  
KEYWORDS EST.

ACCESION BO585399.1 GI:26114981  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herrig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.

REFERENCE  
AUTHORS

## TITLE

CONSTRUCTION OF A 'UNIGENE' cDNA CLONE SET BY OLIGONUCLEOTIDE  
FINGERPRINTING ALLOWS ACCESS TO 25 000 POTENTIAL SUGAR BEET GENES

JOURNAL MEDLINE  
PUBMED 12472698

## COMMENT

ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 1 row: 1 column: 05  
Seq primer: SP6; ATTAGTGACACTATAGAGA.  
Location/Qualifiers  
1..16  
/organism="Beta vulgaris"

FEATURES  
source

## ORIGIN

Alignment Scores:  
Pred. No.: 3.39e+06 Length: 16  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BO585399 (1-16)

QY 132 ALAGLYVAL 134

Db 3 GCTGTGTA 11

## RESULT 179

BO586020 16 bp mRNA linear EST 06-DEC-2002  
LOCUS E012394-024-013-N21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone  
DEFINITION 024-013-N21-5-PRIME, mRNA sequence.  
ACCESSION BO586020  
VERSION BO586020.1 GI:26115602  
KEYWORDS EST.

ACCESION BO586020.1 GI:26115602  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herrig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.

REFERENCE  
AUTHORS

## TITLE

CONSTRUCTION OF A 'UNIGENE' cDNA CLONE SET BY OLIGONUCLEOTIDE  
FINGERPRINTING ALLOWS ACCESS TO 25 000 POTENTIAL SUGAR BEET GENES

JOURNAL MEDLINE  
PUBMED 12472698

## COMMENT

ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 13 row: N column: 21  
Seq primer: SP6; CATACGATTGCTGACACTATAG.  
Location/Qualifiers  
1..16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:186842"

FEATURES  
source

```

/db_xref="taxon:161934"
/clone="024-013-M21"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation: SP6-Sall-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586020 (1-16)

QY 11 PhleuTYR 13
Db 2 TTCTATAT 10

RESULT 180
BQ586219 16 bp mRNA linear EST 06-DEC-2002
LOCUS E012392-024-013-C19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION BQ586219
ACCESSION BQ586219
VERSION BQ586219.1 GI:26115801
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,M., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 13 row: C column: 19
Seq primer: SP6; CATACGATTAGCGACACATATAG.
Location/Qualifiers
1. 16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:186651"
/db_xref="taxon:161934"
/clone="024-013-C19"
/tissue_type="leaf"
/lab_host="EMDH10B"
/lab_host="EMDH10B"

FEATURES
source

```

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/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation: SP6-Sall-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586219 (1-16)

QY 109 PhetHAla 111
Db 10 TTACCGCA 2

RESULT 181
BQ587767 16 bp mRNA linear EST 06-DEC-2002
LOCUS E012340W-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION BQ587767
ACCESSION BQ587767
VERSION BQ587767.1 GI:26117349
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,M., Menze,A., O'Brien,J., Lehnach,H. and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 10 row: M column: 01
Seq primer: SP6; CATACGATTAGCGACACATATAG.
Location/Qualifiers
1. 16
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:185096"
/db_xref="taxon:161934"
/clone="024-010-M01"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation: SP6-Sall-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source

```

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

## ORIGIN

## Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x BQ587767 (1-16)

OY 3 SerLeuLeu 5

Db 2 TCTCTCCTC 10

## RESULT 182

BQ587767 16 bp mRNA linear EST 06-DEC-2002

LOCUS B012340w-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA

DEFINITION clone 024-010-M01 5-PRIME, mRNA sequence.

ACCESSION BQ587767

VERSION BQ587767.1 GI:26117349

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE Caryophyllales; Amaranthaceae; Beta.

JOURNAL 1 (bases 1 to 16)

MEDLINE Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,

PUBMED Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

COMMENT and Radolof,U.

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpi-z-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 10 row: M column: 01

Seq primer: SP6; CATACGATTGAGTGACACTATAG.

Location/Qualifiers

1..16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultiivar="KMS2320 (double haploid, monogerm breeding

line)"

/db\_xref="GABI:185096"

/db\_xref="taxon:161934"

/clone="024-010-M01"

/issue\_type="leaf"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-leaf"

/note="Vector: PCWVSFOR6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Bindeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

## ORIGIN

## Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x BQ587767 (1-16)

OY 24 ArgArgGlu 26

Db 9 AGGAGAGAG 1

## RESULT 183

BQ588093

LOCUS B012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

DEFINITION 024-009-A19 5-PRIME, mRNA sequence.

ACCESSION BQ588093

VERSION BQ588093.1 GI:26117675

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE Caryophyllales; Amaranthaceae; Beta.

JOURNAL 1 (bases 1 to 16)

MEDLINE Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,

PUBMED Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

COMMENT and Radolof,U.

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpi-z-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 9 row: A column: 19

Seq primer: SP6; CATACGATTGAGTGACACTATAG.

Location/Qualifiers

1..16

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/mol\_type="mRNA"

/cultiivar="KMS2320 (double haploid, monogerm breeding

line)"

/db\_xref="GABI:184766"

/db\_xref="taxon:161934"

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/issue\_type="leaf"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-leaf"

/note="Vector: PCWVSFOR6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Bindeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

## ORIGIN

## Alignment Scores:

Pred. No.: 3.39e+06 Length: 16  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ588093 (1-16)

QY 22 TysGlyArg 24

DB 4 AAGGAGGA 12

RESULT 184

BQ588093 16 bp mRNA linear EST 06-DEC-2002  
 LOCUS E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 DEFINITION 024-009-A19 5-PRIME, mRNA sequence.

ACCESSION BQ588093

VERSION BQ588093.1 GI:26117675

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:184766"

/db\_xref="taxon:161934"

/issue\_type="leaf"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatnucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-17; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 1.52% Gaps: 0

Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ588093 (1-16)

QY 42 PheSerLeu 44

DB 13 TTCTCCCTT 5

RESULT 185

BQ588621

LOCUS E012562-024-015-N03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

DEFINITION cDNA clone 024-015-N03 5-PRIME, mRNA sequence.

ACCESSION BQ588621

VERSION BQ588621.1 GI:26118204

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187387"

/db\_xref="taxon:161934"

/clone="024-015-N03"

/issue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatnucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-17; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 1.52% Gaps: 0

US-09-966-880A-8 (1-198) x BQ588621 (1-16)

QY 104 LeuserLeu 106

Db 4 CTTTCTCTC 12

RESULT 186

BQ588621/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 16

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="XMS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187387"

/db\_xref="taxon:161934"

/clone="024-015-N03"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP12-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwiesener Saatgut AG Bindeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCGCGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 13

Db 16 AGGAGAGAG 8

RESULT 187

CF303743

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

RESULT 188

CF306313/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

RESULT 188

CF306313

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

RESULT 188

CF306313

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

RESULT 188

CF306313

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

RESULT 188

CF306313

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli SOLR"

/clone\_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 GYARGARG 25

Db 7 GGGCGGCGC 15

## ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

## TITLE

Large-scale Sequencing Analysis of Rice ESTs

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 321 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1..16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HDAL-03-G11"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library 1 (HDAL1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

## Alignment Scores:

Pred. No.:	3,39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF307345 (1-16)

Oy 38 SerAlaThr 40

Db 10 AGTGCAC 2

## RESULT 189

CF307345/c

LOCUS

DEFINITION

CF307345

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1..16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HDAL-06-H02"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library 1 (HDAL1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

## ORIGIN

## Alignment Scores:

Pred. No.:	3,39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF307345 (1-16)

Oy 70 LeuAppPro 72

Db 14 TTGATCCT 6

## RESULT 190

HSM007757

ID

HSM007757

standard; mRNA; EST, 17 BP.

XX

AC

AL042907;

XX

SV

AL042907.1

XX

DT

12-MAR-1999 (Rel. 59, Created)

XX

DE

Homo sapiens mRNA; EST DKFZP434J1622\_r1 (from clone DKFZP434J1622)

XX

KW

EST; expressed sequence tag.

XX

OS

Homo sapiens (human)

XX

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX

OC

Eutheria; Primates; Catarrhini; Hominidae; Homo.

XX

[1]

1-17

RA

Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

XX

RT

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX

RL

MPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY

XX

CC

Clone from S. Wiemann, sequenced by LMU within the CDNA

XX

CC

sequencing consortium of the German Genome Project

XX

CC

No st sequence available

XX

CC

This clone is available at the RZPD in Berlin

XX

CC

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX

CC

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FH

Key

Location/Qualifiers

FH

source

1..17

FT

/db\_xref="taxon:9606"

FT

/mol\_type="mRNA"

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FT      /organism="Homo sapiens"
FT      /clone="DKFZp434J1622"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     1.52%       Indels:      0
DB:             2           Gaps:        0

US-09-966-880A-8 (1-198) x HSM007757 (1-17)

QY      79 ThrtTpphe 81
Db      3 ACTTGATTC 11

RESULT 191
HSM007757/c      standard; mRNA; EST; 17 BP.
XX
XX      AL042907;
XX      SV      AL042907.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434J1622_r1 (from clone DKFZp434J1622)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPs, Am Klopferersplitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH      Key      Location/Qualifiers
FH
FT      source      1..17
FT      /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434J1622"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     1.52%       Indels:      0
DB:             2           Gaps:        0

US-09-966-880A-8 (1-198) x HSM007757 (1-17)

QY      193 PheArgThr 195
Db      15 TTCGGAACC 7

RESULT 192
HSM007775/c      standard; mRNA; EST; 17 BP.
XX
XX      AL042925;
XX      AC      AL042925.1
XX      SV      AL042925.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434K1222_r1 (from clone DKFZp434K1222)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPs, Am Klopferersplitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH      Key      Location/Qualifiers
FH
FT      source      1..17
FT      /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434K1222"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     1.52%       Indels:      0
DB:             2           Gaps:        0

US-09-966-880A-8 (1-198) x HSM007775 (1-17)

QY      193 PheArgThr 195
Db      13 TTCGGAACC 5

RESULT 193

```

```

Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     1.52%       Indels:      0
DB:             2           Gaps:        0

US-09-966-880A-8 (1-198) x HSM007757 (1-17)

QY      193 PheArgThr 195
Db      15 TTCGGAACC 7

RESULT 192
HSM007775/c      standard; mRNA; EST; 17 BP.
XX
XX      AL042925;
XX      AC      AL042925.1
XX      SV      AL042925.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434K1222_r1 (from clone DKFZp434K1222)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPs, Am Klopferersplitz 18a D-82152 Martinsried, GERMANY
XX
CC      Clone from S. Wiemann, sequenced by LMU within the cDNA
CC      sequencing consortium of the German Genome Project
CC      No s1 sequence available
CC      This clone is available at the RZPD in Berlin
CC      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH      Key      Location/Qualifiers
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FT      source      1..17
FT      /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone="DKFZp434K1222"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     1.52%       Indels:      0
DB:             2           Gaps:        0

US-09-966-880A-8 (1-198) x HSM007775 (1-17)

QY      193 PheArgThr 195
Db      13 TTCGGAACC 5

RESULT 193

```

AM059592/c 17 bp mRNA linear EST 23-AUG-2000  
 LOCUS Hutr.bsc.dnc15.final.cluster\_82\_(3) Dnc15 Homo sapiens cDNA  
 DEFINITION similar to ribosomal protein l12, mRNA sequence.  
 ACCESSION AM059592  
 VERSION AM059592.1 GI:6651914  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 17)  
 BREMER,S., Williams,S.R., Vermase,E.H., Storch,T., Moon,K.,  
 McColium,C., Mao,J.I., Kitchner,J.J., Eletz,S., Dubridge,R.B.,  
 Burcham,T. and Albrecht,G.  
 In vitro cloning of complex mixtures of DNA on microbeads: Physical  
 separation of differentially expressed cDNAs  
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 20144098  
 MEDLINE 10677516  
 PUBMED  
 COMMENT Contact: Burcham TS  
 LYNX Therapeutics, Inc.  
 25861 Industrial Blvd., Hayward, CA 94545, USA  
 Tel: 510 670 9338  
 Fax: 510 670 9302  
 Email: timb@lynxgen.com  
 Sequence obtained from LYNX Therapeutics Megaseq technology.  
 Collected from the down-regulated gate. Consensus sequence of 3  
 sequences in cluster.  
 High quality sequence stop: 17.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /cell\_type="monocytic leukemia"  
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 /clone\_lib="DNC15"  
 /note="Vector: PCR2.1; Cloning of PCR products from  
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 ORIGIN  
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 Pred. No.: 3 61e+06 Length: 17  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-966-880a-8 (1-198) x AM059592 (1-17)  
 QY 32 ValValLys 34  
 |||||  
 14 GTTGTCAA 6  
 RESULT 194  
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 LOCUS 2821879.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821879 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AM246528  
 VERSION AM246528.1 GI:6589521  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 17)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT Other\_ESTs: 2821879.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-r@mail.nih.gov  
 Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.lnl.gov/btrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T identification: patchcut.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 13  
 contiguous PHRED high quality bases following vector sequence. Very  
 Low Quality Sequence: Trace file contained 17 contiguous distinct  
 peaks following vector sequence. Polyadenylation: Based upon the  
 presence of a XhoI site followed by a run of 14 or more T residues  
 at the beginning of the sequence, this cDNA insert was  
 polyadenylated.  
 Plate: LICM7 row: P column: 8  
 High quality sequence stop: 13.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821879"  
 /issue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: Lung; Vector: pONB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3 61e+06 Length: 17  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 10 Gaps: 0  
 US-09-966-880a-8 (1-198) x AM246528 (1-17)  
 QY 15 PhelyAsn 17  
 |||||  
 8 TTTAAAC 16  
 RESULT 195  
 AM246893 17 bp mRNA linear EST 07-JAN-2000  
 LOCUS 2822293.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822293 5',  
 DEFINITION mRNA sequence.  
 ACCESSION AM246893  
 VERSION AM246893.1 GI:6589886  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 17)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Other\_ESTs: 2822293.3prime

Contact: Robert Strausberg, Ph.D.

Email: cga@bs-remail.nih.gov  
Tissue Procurement: DCTD/DRP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: www.bio.liml.gov/bbpr/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 7 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.  
Plate: L1CM9 row: A column: 14  
High quality sequence stop: 7.  
Location/Qualifiers

## FEATURES

source

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1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2822293"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM246893 (1-17)

Qy 196 LeuGlyLeu 198

Db 14 CTCGGCCTC 6

RESULT 196

LOCUS AM247949

DEFINITION 2820605.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820605 3',

LOCUS mRNA sequence.

ACCESSION AM247949

VERSION AM247949.1 GI:6591037

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2820605.5prime

Contact: Robert Strausberg, Ph.D.  
Email: cga@bs-remail.nih.gov  
Tissue Procurement: DCTD/DRP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

## FEATURES

source

```
1..17
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2820605"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM247949 (1-17)

Qy 59 LeuLeuPhe 61

Db 9 TTACTTTT 17

RESULT 197

LOCUS BG926068/c

DEFINITION HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

LOCUS sequence.

ACCESSION BG926068

VERSION BG926068.1 GI:14320591

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2820605.5prime

Contact: Robert Strausberg, Ph.D.  
Email: cga@bs-remail.nih.gov  
Tissue Procurement: DCTD/DRP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@sk.com  
Seq primer: 17.

# FEATURES

source

1..17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/ciseue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

## ORIGIN

### Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BG926068 (1-17)

QY 169 SerValArg 171

Db 12 AGTGTGAGG 4

RESULT 198

BM395339/C

LOCUS 50072-2-8-F06.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM395339  
VERSION BM395339.1 GI:18195392

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: 73.

ORIGIN

### Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00%  
Query Match: 1.52%  
DB: 12  
Gaps: 0

US-09-966-880A-8 (1-198) x BM395339 (1-17)

QY 154 AasnHaglu 156

Db 14 AATCATGAA 6

RESULT 199

BM396258/C

LOCUS 5009-0-19-G03.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM396258  
VERSION BM396258.1 GI:18196311

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: 73.

ORIGIN

### Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM396258 (1-17)

QY 77 ArgValThr 79

Db 12 CCGGTGACT 4

RESULT 200

BM401224/C

LOCUS 5009-0-84-D08.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION BM401224  
VERSION BM401224.1 GI:18201277

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: 73.

ORIGIN

```

REFERENCE
AUTHORS      1 (bases 1 to 17)
              Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E.,
              Pranke,J., and Klobutcher,L.
TITLE        EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
              Seq primer: 13
FEATURES
source       Location/Qualifiers
              1..17
              /organism="Tetrahymena thermophila"
              /mol_type="rRNA"
              /strain="CU428.1"
              /db_xref="taxon:5911"
              /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
              /note="Vector: Bluescript2 SK+; Details on library
              preparation can be found in Chilcoat and Turkewitz (2001)
              Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%         Indels:      0
DB:             12            Gaps:        0
US-09-966-880A-8 (1-198) x BM401224 (1-17)
QY            129 LeuH1AArg 131
Db            17 CTCACACGC 9
RESULT 201
LOCUS        BQ587868              17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION   S013708-024-009-024-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION    BQ587868
VERSION      BQ587868.1 GI:26117450
KEYWORDS     EST.
SOURCE       Beta vulgaris
ORGANISM     Beta vulgaris
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS      1 (bases 1 to 17)
              Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
              and Radclot,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MP1Z
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mplz-koeln.mpg.de
              Insert Length: 17 Std Error: 0.00
              Plate: 9 row: 0 column: 24
              Seq primer: SP6; CATACGATTGAGTGACACTATAG.
              Location/Qualifiers
              1..17
              /organism="Beta vulgaris"
FEATURES
source
              1..17
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/mol_type="rRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184994"
/db_xref="taxon:161934"
/clone_lib="024-009-024"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5Prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
R2PD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN
Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%         Indels:      0
DB:             13            Gaps:        0
US-09-966-880A-8 (1-198) x BQ587868 (1-17)
QY            51 AsnLYGAsn 53
Db            3 AACCAAAAC 11
RESULT 202
LOCUS        BQ590447              17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION   B012839-024-019-005-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION    BQ590447
VERSION      BQ590447.1 GI:26120030
KEYWORDS     EST.
SOURCE       Beta vulgaris
ORGANISM     Beta vulgaris
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS      1 (bases 1 to 17)
              Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
              and Radclot,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MP1Z
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mplz-koeln.mpg.de
              Insert Length: 17 Std Error: 0.00
              Plate: 19 row: 0 column: 05
              Seq primer: SP6; CATACGATTGAGTGACACTATAG.
              Location/Qualifiers
              1..17
              /organism="Beta vulgaris"
              /mol_type="rRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:189664"

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/db_xref="taxon:161934"
/clone="024-019-005"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ590447 (1-17)

QY 172 LeuserArg 174
DB 1 CTCTCTCTC 9

RESULT 203
BQ593528 17 bp mRNA linear EST 06-DEC-2002
LOCUS BQ593528
DEFINITION S015525-024-026-123-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593528
VERSION BQ593528.1 GI:26123111
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 17)
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinbach,M.,
Dzũngowski,M., Stahl,D., Wüch,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant T 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 26 row: 1 column: 23
Seg primer: SP6; CATACGATTAGGTGACACATATG.
location/Qualifiers
1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:193326"
/db_xref="taxon:161934"
/clone="024-026-123"
/tissue_type="developing root"
/lab_host="EMDH10B"

FEATURES
source

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/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ593528 (1-17)

QY 104 LeuserLeu 106
DB 1 CTCTCTCTC 9

RESULT 204
BQ605828 17 bp mRNA linear EST 25-JUN-2002
LOCUS BQ605828
DEFINITION BRY_1399 wheat EST endosperm library Triticum aestivum CDNA 5',
mRNA sequence.
ACCESSION BQ605828
VERSION BQ605828.1 GI:21554934
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 17)
Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
22478026
12590341
Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
location/Qualifiers
1..17
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuana"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

```

US-09-966-880a-8 (1-198) x BQ605828 (1-17)

Qy 56 HisValGlu 58  
Db 3 CATGTCGAA 11

# RESULT 205

BQ605828 17 bp mRNA linear EST 25-JUN-2002  
BQ605828/c  
LOCUS  
DEFINITION BRY 1399 wheat EST endosperm library Triticum aestivum cDNA 5',  
mRNA sequence.

ACCESSION BQ605828.1 GI:21554934  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Triticum aestivum (bread wheat)  
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 17)  
Clarke, B., Lambrecht, M. and Rhee, S. Y.  
Arabidopsis genomic information for interpreting wheat EST  
sequences

JOURNAL  
MEDLINE  
PUBMED  
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)  
12590341

# COMMENT

The Arabidopsis Information Resource  
Carnegie Institution of Washington, Dept. of Plant Biology  
260 Panama Street, Stanford, CA 94305, USA  
Tel: 1 650 325 1521 x 251  
Fax: 1 650 325 3748  
Email: rheesaccma.stanford.edu.  
Location/Qualifiers

FEATURES  
source  
1..17  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Myuna"  
/db\_xref="taxon:4565"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 8, 10 and 12 DPA  
(days post anthesis)"  
/clone\_lib="wheat EST endosperm library"

# ORIGIN

## Alignment Scores:

Pred. No.: 3.61e+06 Length: 17  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ605828 (1-17)

Qy 105 SerLeuArg 107  
Db 15 TCGCTTGA 7

# RESULT 206

CF299737 17 bp mRNA linear EST 15-AUG-2003  
7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-N22, mRNA sequence.

ACCESSION CF299737  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone\_lib="7LEAF--03-N22"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site: 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

# ORIGIN

## Alignment Scores:

Pred. No.: 3.61e+06 Length: 17  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF299737 (1-17)

Qy 25 ArgGluThr 27  
Db 2 CCGGAACA 10

# RESULT 207

CF299737 17 bp mRNA linear EST 15-AUG-2003  
7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-N22, mRNA sequence.

ACCESSION CF299737  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzae; Oryza.

# REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"

/clone="7L2AF--03-N22"  
 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7L2AF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligotibonucleotides and then used as templates for  
 RT-PCR."

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.61e+06	3.00	100.00%	100.00%	1.52*	17	3	0	0	0	0

US-09-966-880A-8 (1-198) x CF299737 (1-17)

QY 16 Lysanval 18  
 Db 15 AAAAAATT 7

## RESULT 208

CF306383 17 bp mRNA linear EST 15-AUG-2003  
 LOCUS HDAL--03-K15.g1 OSHDAC1-overexpressing transgenic rice lambda phage  
 DEFINITION CDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-K15, mRNA  
 sequence.

ACCESSION CF306383  
 VERSION CF306383.1 GI:33678144  
 EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

Location/Qualifiers

1..17

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HDAL--03-K15"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="OSHDAC1-overexpressing transgenic rice lambda  
 phage cDNA library I (HDAL)"  
 /note="Vector: pBluescript SK(+); Site 1: SacI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice histone deacetylase overexpression line."

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Length:	Matches:	Conservative:
3.61e+06	3.00	100.00%	17	3	0

Best Local Similarity: 100.00%  
 Query Match: 1.52\*  
 Db: 14  
 Gaps: 0

US-09-966-880A-8 (1-198) x CF306383 (1-17)

QY 193 Pheargthr 195

Db 1 TTCCGCACC 9

## RESULT 209

CF339347 17 bp mRNA linear EST 18-AUG-2003  
 LOCUS RCL1--04-J13.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 DEFINITION Oryza sativa cDNA clone RCL1--04-J13, mRNA sequence.

ACCESSION CF339347  
 VERSION CF339347.1 GI:33827081  
 EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 17)

REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.-K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gpbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

Location/Qualifiers

1..17

/organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="RCL1--04-J13"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli SOLR"  
 /clone\_lib="Regenerated callus lambda phage cDNA library  
 (RCL1)"  
 /note="Vector: pBluescript SK(+); Site 1: SacI; Site 2:  
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
 end with SacI and 3' end with XhoI site. Callus was  
 induced on 2N6 media for 30 days and cultured for 36hrs on  
 regenerated media"

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.61e+06	3.00	100.00%	100.00%	1.52*	17	3	0	0	0	0

US-09-966-880A-8 (1-198) x CF339347 (1-17)

QY 60 Leupheleu 62

Db 5 CTTTCTCT 13

## RESULT 210

CF921142 17 bp mRNA linear EST 05-NOV-2003  
 LOCUS gmrRw3-05\_H07\_1.049 Soybean root hair subtracted cDNA library  
 DEFINITION gmrRw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF921142  
 VERSION CF921142.1 GI:38191936  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 REFERENCE 1 (bases 1 to 17)  
 Schaeffer, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.  
 Expressed sequence tags from soybean root hair subtractive cDNA library  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Gary Stacey  
 University of Missouri  
 108 Waters Hall, Columbia, MO 65211, USA  
 Tel: 573-884-4752  
 Fax: 573-882-0588  
 Email: stacey@missouri.edu  
 Single pass sequence  
 Seq primer: 17  
 FEATURES  
 source  
 Location/Qualifiers  
 1..17  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Williams 82"  
 /db\_xref="taxon:3847"  
 /tissue\_type="root hairs"  
 /clone\_lib="Soybean root hair subtracted cDNA library gmrhwm3"  
 /note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Brachytrichobium japonicum for 3 hours."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.61e+06 Length: 17  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x CF921142 (1-17)  
 QY 31 TyValVal 33  
 DB 17 TATGTTGTA 9  
 RESULT 211  
 D11808/c 17 bp mRNA linear EST 02-DEC-1992  
 LOCUS HUMEM01H11 Liver HepG2 cell line. Homo sapiens cDNA clone hm01h11,  
 DEFINITION mRNA sequence.  
 ACCESSION D11808  
 VERSION D11808.1 GI:2155083  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 17)  
 Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y. and Matsubara, K.  
 Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression  
 JOURNAL Nat. Genet. 2, 173-179 (1992)  
 MEDLINE 94258199  
 COMMENT Contact: Kouzaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niiyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara  
 Institute for Molecular and Cellular Biology

Osaka University  
 1-3 Yamada-oka, Suita, Osaka 565, Japan.  
 FEATURES  
 source  
 Location/Qualifiers  
 1..17  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:D088354E"  
 /db\_xref="taxon:9606"  
 /clone="hm01h11"  
 /lab\_host="E.coli"  
 /clone\_lib="Liver HepG2 cell line."  
 /note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.61e+06 Length: 17  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0  
 US-09-966-880A-8 (1-198) x D11808 (1-17)  
 QY 185 GIUValASP 187  
 DB 14 GAGGTCGAT 6  
 RESULT 212  
 PCH303755  
 LOCUS Plasmodium chabaudi genome survey sequence, clone PCTc5.plt,  
 DEFINITION genomic survey sequence.  
 ACCESSION AJ303755  
 VERSION AJ303755.1 GI:11140262  
 KEYWORDS GSS; genome survey sequence.  
 SOURCE Plasmodium chabaudi  
 ORGANISM Plasmodium chabaudi  
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 REFERENCE 1 (bases 1 to 17)  
 Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D., Bowman, S., Phillips, R.S. and Turner, C.M.  
 Gene discovery in Plasmodium chabaudi by genome survey sequencing  
 JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)  
 MEDLINE 11295179  
 COMMENT Submitted (06-NOV-2000) Division of Infection & Immunity,  
 University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK  
 bases 39 to 55 (OL to SR).  
 FEATURES  
 source  
 Location/Qualifiers  
 1..17  
 /organism="Plasmodium chabaudi"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:5825"  
 /clone="PCTc5.plt"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.61e+06 Length: 17  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 29 Gaps: 0  
 US-09-966-880A-8 (1-198) x PCH303755 (1-17)  
 QY 113 LeuTYrPhe 115  
 |||||

```

Db          3 CTGTATTT 11

RESULT 213
PCH303755/c 17 bp DNA linear GSS 03-APR-2001
LOCUS      Plasmodium chabaudi genome survey sequence, clone PCTc5.plt.
DEFINITION
ACCESSION  AJ303755
VERSION    AJ303755.1 GI:11140262
KEYWORDS  GSS; genome survey sequence.
SOURCE    Plasmodium chabaudi
ORGANISM  Plasmodium chabaudi
REFERENCE  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
AUTHORS   1 (bases 1 to 17)
          Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
          Bowman,S., Phillips,R.S. and Turner,C.M.
          Gene discovery in Plasmodium chabaudi by genome survey sequencing
JOURNAL    Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE    21125358
PUBMED     11295179
REFERENCE  2 (bases 1 to 17)
AUTHORS   Janssen,C.S.
TITLE      Direct Submission
JOURNAL    Submitted (06-NOV-2000) Division of Infection & Immunity,
          University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
          bases 39 to 55 (QI to SR).
COMMENT    Location/Qualifiers
FEATURES   1..17
            source          /organism="Plasmodium chabaudi"
                           /mol_type="genomic DNA"
                           /db_xref="taxon:5825"
                           /clone="PCTc5.plt"

ORIGIN

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%        Indels:      0
DB:             29           Gaps:       0

US-09-966-880A-8 (1-198) x PCH303755, (1-17)

QY          15 PheLysAsn 17
Db          15 TTTAAAT 7

RESULT 214
HSM004368/c  standard; mRNA; EST, 18 BP.
ID          HSM004368
XX          AC AL039892;
XX          SV AL039892.1
XX          DT 12-MAR-1999 (Rel. 59, Created)
XX          DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX          DE Homo sapiens mRNA; EST DKFZp434G1212_r1 (from clone DKFZp434G1212)
XX          EST; expressed sequence tag.
XX          OS Homo sapiens (human)
XX          OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX          CC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX          RN [1]
XX          RP 1-18
XX          RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX          RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX          RL MIPS, Am Kiopterapitz 18a D-82152 Martinsried, GERMANY

```

```

XX          CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
XX          CC sequencing consortium of the German Genome Project
XX          CC No s1 sequence available
XX          CC This clone is available at the RZPD in Berlin
XX          CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX          CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX          FH Key
XX          FH Location/Qualifiers
XX          FT source
XX          FT 1..18
XX          FT /db_xref="taxon:9606"
XX          FT /mol_type="rRNA"
XX          FT /organism="Homo sapiens"
XX          FT /clone="DKFZp434G1212"
XX          FT /clone_1ib="434 (synonym: hres3). Vector pSport1; host
XX          FT DH10B; sites NotI + SalI"
XX          FT /dev_stage="adult"
XX          FT /issue_type="testis"
XX          SQ Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%        Indels:      0
DB:             2           Gaps:       0

US-09-966-880A-8 (1-198) x HSM004368 (1-18)

QY          193 PheArgThr 195
Db          14 TTCCGACC 6

RESULT 215
HSM007922/c  standard; mRNA; EST, 18 BP.
ID          HSM007922
XX          AC AL043072;
XX          SV AL043072.1
XX          DT 12-MAR-1999 (Rel. 59, Created)
XX          DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX          DE Homo sapiens mRNA; EST DKFZp434B1823_r1 (from clone DKFZp434B1823)
XX          EST; expressed sequence tag.
XX          OS Homo sapiens (human)
XX          OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX          CC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX          RN [1]
XX          RP 1-18
XX          RA Blum H., Buererachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX          RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX          RL MIPS, Am Kiopterapitz 18a D-82152 Martinsried, GERMANY
XX          CC Clone from S. Wiemann, sequenced by LMU within the cDNA
XX          CC sequencing consortium of the German Genome Project
XX          CC No s1 sequence available
XX          CC This clone is available at the RZPD in Berlin
XX          CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX          CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX          FH Key
XX          FH Location/Qualifiers
XX          FT source
XX          FT 1..18
XX          FT /db_xref="taxon:9606"

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FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_id="DKFZp434B1.823"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX      SQ      Sequence 18 bp; 3 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             2            Gaps:        0

US-09-966-880A-8 (1-198) x HSM007922 (1-18)

Qy      193 PheArgThr 195
Db      16 TTCCGACC 8

RESULT 216
LOCUS   AM246505      18 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
          mRNA sequence.
ACCESSION AM246505
VERSION   AM246505.1 GI:6589498
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 18)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          JOURNAL Unpublished (1999)
          Other ESTs: 2821585.5prime
          Contact: Robert Strausberg, Ph.D.
          Email: cgaabbs@mail.nih.gov
          Tissue Procurement: DCTD/DMP CDNA Library Preparation: Ling
          Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
          Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
          Project Clone distribution: MGC clone distribution information can
          be found through the I.M.A.G.E. Consortium/LNL at:
          www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu Low Quality Sequence: 18
          contiguous PHRED high quality bases following vector sequence. Very
          low Quality Sequence: Trace file contained 18 contiguous distinct
          peaks following vector sequence. Polyadenylation: Based upon the
          presence of a XhoI site followed by a run of 14 or more T residues
          at the beginning of the sequence, this cDNA insert was
          polyadenylated.
          Plate: L16M7 row: D column: 2
          High quality sequence stop: 18.
          Location/Qualifiers
            1..18
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:2821585"
              /tissue_type="small cell carcinoma"
              /cell_line="MGC3"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC 7"
              /note="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2:
FEATURES
source
```

```
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcorI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).".

ORIGIN

Alignment Scores:
Pred. No.:      3.83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             10            Gaps:        0

US-09-966-880A-8 (1-198) x AM246505 (1-18)

Qy      42 PheSerLeu 44
Db      7 TTTCTTTA 15

RESULT 217
LOCUS   AM250267      18 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2821151.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821151 5',
          mRNA sequence.
ACCESSION AM250267
VERSION   AM250267.1 GI:6593260
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
          1 (bases 1 to 18)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          JOURNAL Unpublished (1999)
          Other ESTs: 2821151.3prime
          Contact: Robert Strausberg, Ph.D.
          Email: cgaabbs@mail.nih.gov
          Tissue Procurement: DCTD/DMP CDNA Library Preparation: Ling
          Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
          Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
          Project Clone distribution: MGC clone distribution information can
          be found through the I.M.A.G.E. Consortium/LNL at:
          www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
          Scores: PHRED from University of Washington Genome Center. Vector
          Trimming: cross_match from University of Washington Genome Center
          PHRAP suite. Poly-T Identification: patch.pl from Berkeley
          Drosophila Genome Project. University of Washington Genome Center:
          http://www.genome.washington.edu Low Quality Sequence: 16
          contiguous PHRED high quality bases following vector sequence. Very
          low Quality Sequence: Trace file contained 18 contiguous distinct
          peaks following vector sequence.
          Plate: L16M6 row: A column: 24
          High quality sequence stop: 16.
          Location/Qualifiers
            1..18
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:2821151"
              /tissue_type="small cell carcinoma"
              /cell_line="MGC3"
              /lab_host="DH10B (phage-resistant)"
              /clone_lib="NIH MGC 7"
              /note="Organ: Lung; Vector: pOTB7; Site_1: XhoI; Site_2:
FEATURES
source
```

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). "

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). "

## ALIGNMENT SCORES:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x AW250267 (1-18)

QY 23 GIYARGARG 25  
DB 9 GGGAGGCGG 17

## RESULT 218

AW250449 18 bp mRNA linear EST 07-JAN-2000  
LOCUS 2822458.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822458 3',  
DEFINITION mRNA sequence.

ACCESSION AW250449

VERSION AW250449.1 GI:6593442  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2822458.3prime

Contact: Robert Strausberg, Ph.D.  
Email: cga@db-rt@mail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:

www.bio.lnhl.gov/bbip/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 18

contiguous PHRED high quality bases following vector sequence. Very  
low Quality Sequence: trace file contained 18 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was  
polyadenylated.

Plate: L1CM9 row: H column: 11  
High quality sequence stop: 18.

## FEATURES

source

1..18  
Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2822458"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_1ib="NIH\_MGC\_7"

/note="Organ: Lung; Vector: pORF7; Site\_1: XhoI; Site\_2:  
ScorI; cDNA made by oligo-dt priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAAGAG(G) Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of

## ALIGNMENT SCORES:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) x AW250449 (1-18)

QY 42 PhseSerleu 44  
DB 7 TTTTCCCTT 15

## RESULT 219

BG668027 18 bp mRNA linear EST 30-APR-2001  
LOCUS DRABTE12 Rat DRG Library Rattus norvegicus cDNA clone DRABTE12 5',  
DEFINITION mRNA sequence.

ACCESSION BG668027

VERSION BG668027.1 GI:13889949  
KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)  
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,  
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain

Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

JOURNAL MEDLINE  
PUBMED 12060780

COMMENT Contact: Zhang Xu  
Laboratory of Sensory System

Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China

Tel: 86-21-64748700-121  
Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn  
This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shouling Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzegu@ion.sh.cn)

PCR Primers  
FORWARD: T3  
BACKWARD: T7

Seq primer: T3  
POLYA=No.

## FEATURES

source

1..18  
Location/Qualifiers

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="DRABTE12"

/sex="male"

/tissue\_type="dorsal root ganglion"

/dev\_stage="adult"

/clone\_1ib="Rat DRG Library"

## ORIGIN

## ALIGNMENT SCORES:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG668027 (1-18)

Qy 41 Serpentes 43

Db 17 TCTTCTCC 9

RESULT 220

LOCUS BG668047

DEFINITION DRABUA12 Rat DRG library Rattus norvegicus cDNA clone DRABUA12 5', mRNA sequence.

ACCESSION BG668047

VERSION BG668047.1 GI:13889969

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 18)

Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.T., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

AUTHORS

JOURNAL

MEDLINE

PUBMED

22056133

12060780

COMMENT

CONTACT: Zhang Xu

Laboratory of Sensory System

Institute of Neuroscience

320 Yue Yang Road, Shanghai 200031, P.R. China

Tel: 86-21-64748700-121

Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome

Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,

Pudong New Area, P.R.China. Please contact with Zhang Xu

(xu.zhang@ion.ac.cn) or Han Zeguang (hanzegu@ion.sh.cn)

PCR Primers

FORWARD: T3

BACKWARD: T3

Seq primer: T3

POLYA=No.

FEATURES

source

1. .18

Location/Qualifiers

/organism="Rattus norvegicus"

/mol\_type="mRNA"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="DRABUA12"

/sex="male"

/tissue\_type="dorsal root ganglion"

/dev\_stage="adult"

/clone\_lib="Rat DRG Library"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG668047 (1-18)

Qy 104 LeuSerLeu 106

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|||||

Db 2 CTCCTCTC 10

RESULT 221

LOCUS BG896958

DEFINITION HOA59-1-D4.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG896958

VERSION BG896958.1 GI:14307199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 18)

Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Iark,M.W.

AUTHORS

JOURNAL

MEDLINE

PUBMED

21482651

11597177

COMMENT

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7

FEATURES

source

1. .18

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="Cartilage"

/lab\_host="E.coli DH10 B"

/clone\_lib="HOA (Human Osteoarthritic Cartilage)"

/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG896958 (1-18)

Qy 180 LeuLeuPro 182

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TITLE  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries

JOURNAL  
MEDLINE  
PUBMED  
21482651  
11597177  
Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@sk.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1..18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HOA (Human Osteochondritic Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG90971 (1-18)

QY 23 GYARGATG 25  
|||||  
11 GCGAGGAGG 3

Db  
RESULT 223  
BG900971 18 bp mRNA linear EST 06-NOV-2001  
LOCUS HOA52-1-C2.R HOA (Human Osteochondritic Cartilage) Homo sapiens  
DEFINITION CDNA, mRNA sequence.  
ACCESSION BG900971  
VERSION BG900971.1 GI:14311220  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mull,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177  
Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@sk.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1..18

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG900971 (1-18)

QY 105 SerLeuArg 107  
|||||  
5 TCCTTAGGC 13

Db  
RESULT 224  
BG924473 18 bp mRNA linear EST 06-NOV-2001  
LOCUS HNC27-1-D2.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA  
DEFINITION sequence.  
ACCESSION BG924473  
VERSION BG924473.1 GI:14318996  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathe,G., Mull,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.  
Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries  
Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
21482651  
11597177  
Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@sk.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1..18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG924473 (1-18)

QY 112 ArgLeuTyr 114  
Db 2 AGACTCTAT 10

RESULT 225 BG924473 18 bp mRNA linear EST 06-NOV-2001  
LOCUS BG924473/c HNC27-1-D2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
DEFINITION sequence..

ACCESSION BG924473  
VERSION BG924473.1 GI:14318996  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PubMed 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsk.com

Seq primer: T7.  
Location/Qualifiers

FEATURES  
source 1..18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

# ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 0

DB: 12  
US-09-966-880a-8 (1-198) x BG924473 (1-18)

QY 76 TyrArgVal 78  
Db 11 TTAGAGTC 3

RESULT 226

LOCUS BG925410 18 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC5-1-B6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence..

ACCESSION BG925410  
VERSION BG925410.1 GI:14319933  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 (bases 1 to 18)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PubMed 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay.kumar-1@gsk.com  
Seq primer: T7.  
Location/Qualifiers

## FEATURES

source 1..18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
Gaps: 0

DB: 12  
US-09-966-880a-8 (1-198) x BG925410 (1-18)

QY 104 LeuSerLeu 106  
Db 4 CTCTCCCTA 12

RESULT 227

LOCUS BG925569 18 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC5-1-B2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence..

ACCESSION BG925569  
VERSION BG925569.1 GI:14320092  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
MEDLINE 21482651  
PubMed 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245

Fax: 610-270-5598  
Email: sanjay\_kumar-1@gsf.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1. .18  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG925569 (1-18)

QY 181 LeuProLeu 183

Db 4 CTCCTCCTC 12

RESULT 228  
LOCUS BG925569/c 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC5-1-E2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG925569.1 GI:14320092

VERSION BG925569.1

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries

JOURNAL 21482651  
MEDLINE 21482651  
PUBMED 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay\_kumar-1@gsf.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1. .18  
/organism="Homo sapiens"  
/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG927414 (1-18)

QY 59 LeuProLeu 61

Db 2 CTCCTCCTC 10

RESULT 230  
LOCUS BG927414/c 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG927414.1 GI:14321937

VERSION BG927414.1

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.

Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG925569 (1-18)

QY 24 ArgArgGlu 26

Db 18 AGAGAGGAG 10

RESULT 229  
LOCUS BG927414

DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG927414.1 GI:14321937

VERSION BG927414.1

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries

JOURNAL 21482651  
MEDLINE 21482651  
PUBMED 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay\_kumar-1@gsf.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
source  
1. .18  
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/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
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/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG927414 (1-18)

QY 59 LeuProLeu 61

Db 2 CTCCTCCTC 10

RESULT 230  
LOCUS BG927414/c 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG927414.1 GI:14321937

VERSION BG927414.1

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)  
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed  
sequenced tags (ESTs) each from adult human normal and  
osteochondritic cartilage cDNA libraries

JOURNAL 21482651  
MEDLINE 21482651  
PUBMED 11597177

COMMENT Contact: Sanjay Kumar  
UM2109  
GlaxoSmithKline  
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
Tel: 610-270-7245  
Fax: 610-270-5598  
Email: sanjay\_kumar-1@gsf.com  
Seq primer: T7,  
Location/Qualifiers

FEATURES  
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/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="cartilage"  
/lab\_host="E.coli DH10 B"  
/clone\_lib="HNC (Human Normal Cartilage)"  
/note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
Directional"

ORIGIN  
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Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG927414 (1-18)

QY 59 LeuProLeu 61

Db 2 CTCCTCCTC 10

RESULT 230  
LOCUS BG927414/c 18 bp mRNA linear EST 06-NOV-2001  
DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
sequence.

ACCESSION BG927414 GI:14321937  
 VERSION BG927414.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 18)  
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathie, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and Larr, M.W.  
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 JOURNAL MEDLINE  
 PUBMED 21482651  
 11597177  
 Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-1@gsk.com  
 Seq primer: T7.  
 Location/Qualifiers  
 1..18  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
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 /lab\_host="E.coli DH10 B"  
 /clone\_lib="VNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: Salt; Site\_2: Not; Directional"  
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 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880A-8 (1-198) x BG927414 (1-18)  
 QY 24 ArgArgGlu 26  
 |||||  
 11 AGAAGAGAA 3  
 RESULT 231  
 BM394601 18 bp mRNA linear EST 17-JAN-2002  
 LOCUS 50072-2-5-B10.r.1 Chlicoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM394601  
 VERSION BM394601.1 GI:18194654  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
 1 (bases 1 to 18)  
 Turkewitz, A.P., Karier, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 DB: 12 Gaps: 0  
 TITLE JOURNAL  
 COMMENT Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 DB: 12 Gaps: 0

Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
 1..18  
 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0  
 US-09-966-880A-8 (1-198) x BM394601 (1-18)  
 QY 177 ArgArgGile 179  
 |||||  
 2 CGCCGTATA 10  
 RESULT 232  
 BM394638 18 bp mRNA linear EST 17-JAN-2002  
 LOCUS 50072-2-5-B10.r.1 Chlicoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.  
 ACCESSION BM394638  
 VERSION BM394638.1 GI:18194691  
 KEYWORDS EST.  
 SOURCE Tetrahymena thermophila  
 ORGANISM Tetrahymena thermophila  
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.  
 1 (bases 1 to 18)  
 Turkewitz, A.P., Karier, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J. and Klobutcher, L.  
 EST from Tetrahymena thermophila, strain CU428.1, growing cells  
 Unpublished (2002)  
 Contact: Turkewitz AP  
 Molecular Genetics and Cell Biology  
 University of Chicago  
 920 E. 58th Street, Chicago, IL 60637, USA  
 Tel: 773 702 4374  
 Fax: 773 702 3172  
 Email: apturkew@midway.uchicago.edu  
 Seq primer: T3.  
 Location/Qualifiers  
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 /organism="Tetrahymena thermophila"  
 /mol\_type="mRNA"  
 /strain="CU428.1"  
 /db\_xref="taxon:5911"  
 /clone\_lib="Chlicoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."  
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 Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM394638 (1-18)

Qy 129 LeuHISArg 131  
18 CTCGACCGC 10

RESULT 233

BM395123

LOCUS 50072-2-7-F05.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM395123

VERSION

BM395123.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Turkewitz AP

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Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_1ib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 12

Gaps: 0

US-09-966-880A-8 (1-198) x BM395123 (1-18)

Qy 19 ArgTPala 21

2 CGATGGGCT 10

RESULT 234

BM397227

LOCUS 5009-0-3-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)  
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397227

VERSION

BM397227.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_1ib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 12

Gaps: 0

US-09-966-880A-8 (1-198) x BM397227 (1-18)

Qy 77 ArgValThr 79

10 CGCGTACT 2

RESULT 235

BM397853

LOCUS 5009-0-38-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397853

VERSION

BM397853.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

/db\_xref="taxon:5911"

/clone\_1ib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 12

Gaps: 0

US-09-966-880A-8 (1-198) x BM397227 (1-18)

Qy 77 ArgValThr 79

10 CGCGTACT 2

RESULT 235

BM397853

LOCUS 5009-0-38-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397853

VERSION

BM397853.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/strain="CU428.1"

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/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52*	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM397853 (1-18)

QY	58	GluLeuLeu 60
Db	9	GAGCTCCTT 1

RESULT 236  
BM398017/c  
DEFINITION  
5009-0-4-D05.t.1 Chllocoat/Turkewitz cDNA (large fraction)  
Tertrahymena thermophila cDNA, mRNA sequence.

ACCESSION  
BM398017  
VERSION  
BM398017.1 GI:18198070  
SOURCE  
EST.  
ORGANISM  
Tertrahymena thermophila  
Tertrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tertrahymenina; Tertrahymena.  
1 (bases 1 to 18)  
Turkewitz,A.P., Karer,K.M., Jahn,C., Oriae,E., Kirk,K.E.,  
Frankel,J. and Klobutcher,L.  
EST from Tertrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

FEATURES  
source  
Location/Qualifiers  
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/organism="Tertrahymena thermophila"  
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preparation can be found in Chllocoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN  
Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52\* Indels: 0  
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398017 (1-18)

QY	24	ArgArgGln 26
Db	13	CGGGCGGAG 5

RESULT 237  
BM398577  
DEFINITION  
5009-0-47-C10.t.1 Chllocoat/Turkewitz cDNA (large fraction)  
Tertrahymena thermophila cDNA, mRNA sequence.

ACCESSION  
BM398577  
VERSION  
BM398577.1 GI:18198630  
KEYWORDS  
EST.

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52*	Indels:	0
DB:	12	Gaps:	0

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SOURCE
ORGANISM Tetrahymena thermophila
REFERENCE Tetrahymena thermophila
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
1 (bases 1 to 18) Hymenostomatida; Tetrahymenina; Tetrahymena.
TITLE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.B.,
JOURNAL Frankel,J. and Klobutcher,L.
COMMENT EST from Tetrahymena thermophila, strain CU428.1, growing cells
unpublished (2002)
CONTACT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
UNIVERSITY University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
TEL: 773 702 4374
FAX: 773 702 3172
EMAIL: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
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/strain="CU428.1"
/db_xref="taxon:5911"
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/clone="Vector: Bluescript SK+; Details on library
preparation can be found in Chlicoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0
US-09-966-880A-8 (1-198) x BM398577 (1-18)
CY 120 Lysalaglu 122
Db 2 AAAGCGGAG 10
RESULT 238
BM401236 18 bp mRNA linear EST 17-JAN-2002
LOCUS BM401236
DEFINITION 5009-0-84-E12.t.1 Chlicoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM401236
VERSION BM401236.1 GI:18201289
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
REFERENCE Tetrahymena thermophila
AUTHORS Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
1 (bases 1 to 18) Hymenostomatida; Tetrahymenina; Tetrahymena.
TITLE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.B.,
JOURNAL Frankel,J. and Klobutcher,L.
COMMENT EST from Tetrahymena thermophila, strain CU428.1, growing cells
unpublished (2002)
CONTACT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
UNIVERSITY University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
TEL: 773 702 4374
FAX: 773 702 3172
EMAIL: apturkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
FEATURES
SOURCE

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/db\_xref="taxon:5911"  
 /clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
 /note="Vector: Bluescript SK+; Details on library  
 preparation can be found in Chilcoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

## Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM401236 (1-18)

QY 77 ArgValThr 79

DB 3 CGAGTCACG 11

## RESULT 239

BM401236 18 bp mRNA linear EST 17-JAN-2002  
 LOCUS 5009-0-84-B12.c.1 Chilcoat/Turkewitz cDNA (large fraction)  
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM401236.1 GI:18201289

VERSION EST.

KEYWORDS Tetrahymena thermophila

SOURCE Tetrahymena thermophila

ORGANISM Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

REFERENCE 1 (bases 1 to 18)

AUTHORS Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E.,

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells

JOURNAL Unpublished (2002)

COMMENT Contact: Turkewitz AP

CONTACT: Molecular Genetics and Cell Biology

UNIVERSITY OF CHICAGO

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3

FEATURES

Location/Qualifiers

1..18

/organism="Tetrahymena thermophila"

/mol\_type="mRNA"

/db\_xref="taxon:5911"

/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM401236 (1-18)

QY 77 ArgValThr 79

DB 13 CGCGTACG 5

RESULT 240

BM675715/c  
 LOCUS BM675715 18 bp mRNA linear EST 27-FEB-2002  
 DEFINITION TOH602767971.R1 CSEQFXL35 adipose Sus scrofa cDNA, mRNA sequence.  
 ACCESSION BM675715  
 VERSION BM675715.1 GI:18985613

## ORIGIN

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM675715 (1-18)

QY 129 LeuHisArg 131

DB 16 CTCACCGC 8

## RESULT 241

BM675715 18 bp mRNA linear EST 06-DEC-2002  
 LOCUS E011887-024-004-L12-SP6 MP12-AD19-024-inflorescence Beta vulgaris  
 DEFINITION cDNA clone 024-004-L12 5-PRIME, mRNA sequence.

ACCESSION BM675715.1 GI:26113417

VERSION EST.

KEYWORDS Beta vulgaris

SOURCE Beta vulgaris

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 18)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,

TITLE Construction of a 'uniGene' cDNA clone set by oligonucleotide

JOURNAL Plant J. 32 (5), 845-857 (2002)

COMMENT Fingerprinting allows access to 25 000 potential sugar beet genes

PUBMED 12472698

FEATURES

Location/Qualifiers

1..18

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9623"

/clone\_lib="CSEQFXL35 adipose"

/note="Organ: adipose tissue; Vector: pBluescript SK+;

Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert

(5'-NNN...NNNInsert)

CGGATTGAGCTCCACCGCGTGGCGCGCGGCGTGGAG. Sequence 3' of

the inserts (AGGATTCGATTCGACCTTATCGATTCGATTCGATTCGAG.

non-normalized library, sequenced 3' with M13R primer."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM675715 (1-18)

QY 129 LeuHisArg 131

DB 16 CTCACCGC 8

RESULT 241

BM675715 18 bp mRNA linear EST 06-DEC-2002

LOCUS E011887-024-004-L12-SP6 MP12-AD19-024-inflorescence Beta vulgaris

DEFINITION cDNA clone 024-004-L12 5-PRIME, mRNA sequence.

ACCESSION BM675715.1 GI:26113417

VERSION EST.

KEYWORDS Beta vulgaris

SOURCE Beta vulgaris

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 18)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,

TITLE Construction of a 'uniGene' cDNA clone set by oligonucleotide

JOURNAL Plant J. 32 (5), 845-857 (2002)

COMMENT Fingerprinting allows access to 25 000 potential sugar beet genes

PUBMED 12472698

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 18 Std Error: 0.00  
Plate: 4 row: L column: 12  
Seq primer: SP6; CATACATTTAGTGACTAG.

## FEATURES

## source

1. .18  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:182866"  
/db\_xref="taxon:161934"  
/clone="024-004-E13"  
/tissue\_type="inflorescence"  
/lab\_host="EMD108"  
/clone\_id="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ583840 (1-18)

Cy 59 Leupleup 61  
|||||  
6 CTGCTCTT 14

## RESULT 242

BQ584794 18 bp mRNA linear EST 06-DEC-2002  
LOCUS BQ584794  
DEFINITION E011673-024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris  
CDNA clone 024-002-E13 5-PRIME, mRNA sequence.

ACCESSION BQ584794  
VERSION BQ584794.1 GI:26114371  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

## REFERENCE

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 18)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnrich,H. and Radelet,U.  
Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

## TITLE

JOURNAL MEDLINE  
22362189

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

## FEATURES

## source

Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 18 Std Error: 0.00  
Plate: 2 row: E column: 13  
Seq primer: SP6R; ATTAGTGACTAGTAGAGA.  
Location/Qualifiers  
1. .18  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:181907"  
/db\_xref="taxon:161934"  
/clone="024-002-E13"  
/tissue\_type="inflorescence"  
/lab\_host="EMD108"  
/clone\_id="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saat-zucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ584794 (1-18)

Cy 196 Lengylleu 198  
|||||  
10 TTGGGCTTG 18

## RESULT 243

BQ584794 18 bp mRNA linear EST 06-DEC-2002  
LOCUS BQ584794/c  
DEFINITION E011673-024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris  
CDNA clone 024-002-E13 5-PRIME, mRNA sequence.

ACCESSION BQ584794  
VERSION BQ584794.1 GI:26114371  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

## REFERENCE

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 18)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnrich,H. and Radelet,U.  
Construction of a 'unigenes' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

## TITLE

JOURNAL MEDLINE  
22362189

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 18 Std Error: 0.00  
Plate: 2 row: E column: 13

FEATURES  
Seq primer: SP6; ATTAGTGACACTATAGAGA.  
Location/Qualifiers

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1.18
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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:181907"
/db_xref="taxon:161934"
/clone="024-002-El3"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
```

## ORIGIN

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ584794 (1-18)

QY 101 AsnProAsn 103  
|||||

Db 17 AACCCCAT 9

## RESULT 244

BQ586069 18 bp mRNA linear EST 06-DEC-2002  
LOCUS BQ586069  
DEFINITION E01394-024-013-B09-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-013-B09 5-PRIME, mRNA sequence.

ACCESSION BQ586069  
VERSION BQ586069.1 GI:26115651  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)  
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radloff,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert length: 18 Std Error: 0.00  
Plate: 13 row: B column: 09  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
Location/Qualifiers

FEATURES  
source  
1.18  
/organism="Beta vulgaris"

## ORIGIN

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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186792"
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/clone="024-013-B09"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
```

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586069 (1-18)

QY 52 LysAsnGly 54  
|||||

Db 9 AAAATGCA 17

## RESULT 245

BQ586393 18 bp mRNA linear EST 06-DEC-2002  
LOCUS BQ586393  
DEFINITION S01468-024-013-P11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-013-P11 5-PRIME, mRNA sequence.

ACCESSION BQ586393  
VERSION BQ586393.1 GI:26115965  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)  
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radloff,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weishaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weishaar@mpiz-koeln.mpg.de  
Insert length: 18 Std Error: 0.00  
Plate: 13 row: P column: 11  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
Location/Qualifiers

FEATURES  
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line)"  
/db\_xref="GABI:186486"

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/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

```

## ORIGIN

## Alignment Scores:

Pred. No.:	3	83e+06	Length:	18
Score:	3.00	Matches:	3	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	1.52%	Indels:	0	
DB:	13	Gaps:	0	

US-09-966-880A-8 (1-198) x BQ586393 (1-18)

Qy 107 Argillepe 109

Db 1 CGTATCTTC 9

RESULT 246

BQ586393/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

```

18 bp mRNA linear EST 06-DEC-2002
S014468-024-013-P11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-P11 5-PRIME, mRNA sequence.
BQ586393.1 GI:26115965
EST.
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radeleof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 13 row: P column: 11
Seq primer: SP6; CATACGATTGAGTGACACTATAG.
Location/Qualifiers
1..18
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/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186486"
/db_xref="taxon:161934"
/clone="024-013-P11"
/tissue_type="leaf"
/lab_host="EMDH10B"

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/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

```

## ORIGIN

## Alignment Scores:

Pred. No.:	3	83e+06	Length:	18
Score:	3.00	Matches:	3	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	1.52%	Indels:	0	
DB:	13	Gaps:	0	

US-09-966-880A-8 (1-198) x BQ586393 (1-18)

Qy 22 LysGlyArg 24

Db 13 AACGGAAGA 5

RESULT 247

BQ589347

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

```

18 bp mRNA linear EST 06-DEC-2002
S014007-024-015-A02-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-015-A02 5-PRIME, mRNA sequence.
BQ589347.1 GI:26118930
EST.
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radeleof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
12472698
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 15 row: A column: 02
Seq primer: SP6; CATACGATTGAGTGACACTATAG.
Location/Qualifiers
1..18
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/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

```

h.schulz@kws.de; cloning sites Sali-Noti, primer sites and orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-BEET  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

# ORIGIN

Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Qy 42 PhaseLen 44  
 Db 4 TTTTCACTT 12

RESULT 248  
 BQ591606  
 LOCUS 18 bp mRNA linear EST 06-DEC-2002  
 DEFINITION BQ591606-024-017-G11-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-017-G11 5-PRIME, mRNA sequence.

ACCESSION BQ591606  
 VERSION BQ591606.1 GI:26121189  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE AUTHORS  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp1z-koeln.mpg.de  
 Insert Length: 18 Std Error: 0.00  
 Plate: 17 row: G column: 11  
 Seq primer: SP6; CATACGATTGAGTGACACTATAG.  
 Location/Qualifiers  
 1..18

## FEATURES

source  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:188509"  
 /db\_xref="taxon:161934"  
 /clone="024-017-G11"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH108"  
 /clone\_1ib="MP1Z-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener SaatZucht AG Bindeck, Germany; contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-BEET  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

# ORIGIN

Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Qy 42 PhaseLen 44  
 Db 4 TTTTCACTT 12

RESULT 248  
 BQ594437  
 LOCUS 18 bp mRNA linear EST 06-DEC-2002  
 DEFINITION BQ594437-024-024-M20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 CDNA clone 024-024-M20 5-PRIME, mRNA sequence.

ACCESSION BQ594437  
 VERSION BQ594437.1 GI:26124020  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

REFERENCE AUTHORS  
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mp1z-koeln.mpg.de  
 Insert Length: 18 Std Error: 0.00  
 Plate: 24 row: M column: 20  
 Seq primer: SP6; CATACGATTGAGTGACACTATAG.  
 Location/Qualifiers  
 1..18

## FEATURES

source  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:192416"  
 /db\_xref="taxon:161934"  
 /clone="024-024-M20"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH108"  
 /clone\_1ib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener SaatZucht AG Bindeck, Germany; contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-BEET  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

## ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.83e+06	3.00	100.00%	100.00%	1.52%	18	3	0	0	0	0

US-09-966-880A-8 (1-198) x BQ594437 (1-18)

QY 104 Leusertleu 106  
 18 CTCCTCTCTA 10

RESULT 250  
 BQ790001 18 bp mRNA linear EST 30-JUL-2002  
 hage005ah02 Heterobasidion annosum - Scots pine infection stage  
 (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion  
 annosum cDNA clone hage005ah02, mRNA sequence.

ACCESSION BQ790001  
 VERSION BQ790001.1 GI:22004963  
 KEYWORDS EST.  
 SOURCE Pinus sylvestris/Heterobasidion annosum  
 ORGANISM Pinus sylvestris/Heterobasidion annosum  
 Eukaryota; mixed EST libraries.  
 1 (bases 1 to 18)  
 Asiegbu, F.O., Nahalkova, J. and Dean, R.A.  
 Selected Expressed sequence tags of cDNA clones from the  
 interaction of the root rot fungus (Heterobasidion annosum) with  
 seedling roots of Scots pine (Pinus sylvestris)  
 Unpublished (2001)  
 JOURNAL Contract: Fred O. Asiegbu  
 COMMENT Dept. of Forest Mycology & Pathology  
 Swedish University of Agriculture, Box 7026, S-750 07, Uppsala,  
 Sweden  
 Tel: +46 18 67 15 98  
 Fax: +46 18 30 92 45  
 Email: Fred.Asiegbu@kropat.slu.se  
 Seq primer: 17 primer.  
 Location/Qualifiers  
 1..18  
 /organism="Pinus sylvestris/Heterobasidion annosum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:169015"  
 /clone="hage005ah02"  
 /dev\_stage="Seedling roots of scots pine were infected for  
 6 days with H. annosum"  
 /clone\_lib="Heterobasidion annosum - Scots pine infection  
 stage (HAGE) subtraction cDNA library"  
 /note="Vector: pT-Adv; Site: 1: EcoRI; The subtractive  
 hybridization cDNA library was constructed from scots pine  
 roots infected for 6-days with mycelia of Heterobasidion  
 annosum (Fps)."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.83e+06	3.00	100.00%	100.00%	1.52%	18	3	0	0	0	0

US-09-966-880A-8 (1-198) x BQ790001 (1-18)

QY 58 Gluenteleu 60  
 6 GAGCTGCTC 14

RESULT 251  
 C00629

LOCUS C00629 18 bp mRNA linear EST 31-DEC-2002  
 HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA  
 sequence.

ACCESSION C00629  
 VERSION C00629.1 GI:1432859  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 18)  
 Okubo, K.  
 BodyMap: human gene expression database  
 Unpublished (1995)  
 CONTACT: Okubo, K.  
 INSTITUTE for Molecular and Cellular Biol  
 Osaka University  
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111 (ex.3315)  
 Email: kousaku@imcb.osaka-u.ac.jp  
 We are not submitting the same cDNA sequence redundantly to DBJ  
 since 1993. For the abundance information of clones with this  
 sequence in this library and as well as in other 3'-directed  
 libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The  
 sequences of the clones represented by this GS sequences is also  
 found there.

FEATURES  
 source Location/Qualifiers  
 1..18  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="adult"  
 /clone\_lib="Human adult (K.Okubo)"  
 /note="One or more human adult tissue"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.83e+06	3.00	100.00%	100.00%	1.52%	18	3	0	0	0	0

US-09-966-880A-8 (1-198) x C00629 (1-18)

QY 179 Ileleuleu 181  
 2 ATCTTGCTG 10

RESULT 252  
 C01086  
 C01086/c

LOCUS C01086 18 bp mRNA linear EST 31-DEC-2002  
 HUMGS0007743 Human adult (K.Okubo) Homo sapiens cDNA, mRNA  
 sequence.

ACCESSION C01086  
 VERSION C01086.1 GI:1433316  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 18)  
 Okubo, K.  
 BodyMap: human gene expression database  
 Unpublished (1995)  
 CONTACT: Okubo, K.  
 INSTITUTE for Molecular and Cellular Biol  
 Osaka University  
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
 Tel: 06-877-5111 (ex.3315)  
 Email: kousaku@imcb.osaka-u.ac.jp  
 We are not submitting the same cDNA sequence redundantly to DBJ

since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

#### FEATURES

source

1..18  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

#### ORIGIN

##### Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880a-8 (1-198) x C01086 (1-18)

Qy 32 ValValVal 34

DB 14 GTGTCAAA 6

#### RESULT 253

C20904 18 bp mRNA linear EST 31-DEC-2002  
HUMGS0004983 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA  
sequence.

ACCESSION C20904.1 GI:1622014

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS Okubo,K.

TITLE BodyMap: human gene expression database

JOURNAL Unpublished (1995)

COMMENT Contact: Okubo,K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111(ex.3315)  
Email: kouzakui@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

#### FEATURES

source

1..18  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

#### ORIGIN

##### Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0

DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x C20904 (1-18)

Qy 178 ArgileLeu 180

DB 5 AGGATCTCTC 13

#### RESULT 254

C21336 18 bp mRNA linear EST 31-DEC-2002  
HUMGS000372 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA  
sequence.

ACCESSION C21336.1 GI:1622446

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS Okubo,K.

TITLE BodyMap: human gene expression database

JOURNAL Unpublished (1995)

COMMENT Contact: Okubo,K.  
Institute for Molecular and Cellular Biol  
Osaka University  
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan  
Tel: 06-877-5111(ex.3315)  
Email: kouzakui@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

#### FEATURES

source

1..18  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="adult"  
/clone\_lib="Human adult (K.Okubo)"  
/note="One or more human adult tissue"

#### ORIGIN

##### Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880a-8 (1-198) x C21336 (1-18)

Qy 31 TyrValVal 33

DB 7 TATGTGTG 15

#### RESULT 255

CA851280 18 bp mRNA linear EST 01-AUG-2003  
CA851280/c D12A08 B20.02 ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
cDNA clone D12A08 5', mRNA sequence.

ACCESSION CA851280.1 GI:33388073

VERSION EST.

KEYWORDS Glycine max (soybean)

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

```

REFERENCE
AUTHORS      1 (bases 1 to 18)
TITLE        Alkharouf, N.W., Khan, R. and Matthews, B.F.
JOURNAL      Analysis of expressed sequence tags from roots of resistant soybean
COMMENT      infected by the soybean cyst nematode
              Unpublished (2002)
              Contact: Alkharouf, N.W.
              Soybean Genomics and Improvement Laboratory (SGIL)
              US Department of Agriculture (USDA), ARS, PSI
              Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
              USA
              Tel: 301 504 5750
              Fax: 301 504 5728
              Email: alkharouf@ars.usda.gov.
FEATURES
source       Location/Qualifiers
              1..18
              /organism="Glycine max"
              /mol_type="mRNA"
              /cultivar="Peking"
              /db_xref="taxon:3847"
              /clone="D12A08"
              /issue_type="Roots"
              /dev_stage="Seedlings"
              /clone_1ib="cDNA Peking library 2, 4 day SCN3"
              /note="Vector: pBluescript SK-; cDNA clones from mRNA
              extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Alignment Scores:
Pred. No.:      3 83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:          0
DB:             14          Gaps:            0

US-09-966-880A-8 (1-198) x CA851280 (1-18)

Qy           172 LeuserArg 174
Db           12 CTNCTCTGT 4

RESULT 256
LOCUS       CA851607                      18 bp      mRNA      linear      EST 01-AUG-2003
DEFINITION  D15F01 K13.11.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION   CA851607
VERSION     CA851607.1 GI:333884400
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
            1 (bases 1 to 18)
            Alkharouf, N.W., Khan, R. and Matthews, B.F.
            Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
            Unpublished (2002)
            Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharouf@ars.usda.gov.
FEATURES
source       Location/Qualifiers
              1..18
              /organism="Glycine max"
              /mol_type="mRNA"

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/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D15F01"
/issue_type="Roots"
/dev_stage="Seedlings"
/clone_1ib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Alignment Scores:
Pred. No.:      3 83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:          0
DB:             14          Gaps:            0

US-09-966-880A-8 (1-198) x CA851607 (1-18)

Qy           164 GlyLeuHis 166
Db           2 GGGCTACAT 10

RESULT 257
LOCUS       CD486685                      18 bp      mRNA      linear      EST 01-JUL-2003
DEFINITION  CRHS.3A10 Cotton Root and Hypocotyl Lambda ZIPLOX Library (CRH)
ACCESSION   CD486685
VERSION     CD486685.1 GI:31407650
KEYWORDS    EST.
SOURCE      Gossypium hirsutum (upland cotton)
ORGANISM    Gossypium hirsutum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
            1 (bases 1 to 18)
            Dowd, C., Wilson, J. and McFadden, H.
            Different Gene Expression Responses in Cotton Root and Hypocotyl
            tissues during infection with Fusarium Wilt Disease
            Unpublished (2003)
            Contact: Cairtriona Dowd, Helen McFadden
            Commonwealth Scientific and Industrial Research Organisation
            Division of Plant Industry
            Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
            Black Mountain, Canberra, ACT, 2601, Australia
            Tel: 61 2 6246 4914, 6246 5377
            Fax: 61 2 6246 5000
            Email: Cairtriona.Dowd@csiro.au, Helen.McFadden@csiro.au
            Vector clipped sequences Baees 1-17 (GTGACCCACGCGTCCG): SalI
            adapter
            Seq primer: M13 reverse primer
            High quality sequence stop: 18.
            Location/Qualifiers
              1..18
              /organism="Gossypium hirsutum"
              /mol_type="mRNA"
              /cultivar="DeltaEMERALD"
              /db_xref="taxon:3635"
              /clone="CRHS.3A10"
              /issue_type="Root and hypocotyl tissues"
              /dev_stage="5 day old seedlings"
              /lab_host="Y1090(ZL)"
              /clone_1ib="Cotton Root and Hypocotyl Lambda ZIPLOX
              library (CRH)"
              /note="Vector: Lambda ZIPLOX; Site 1: SalI; Site 2: NotI;
              mRNA was prepared from root and hypocotyl tissues of the
              cotton cultivar DeltaEMERALD. cDNA was synthesised from a
              NotI-oligodT primer/adaptor using the manufacturers
              protocols (Life Technologies) and then ligated to a SalI
              adapter to facilitate directional cloning. The cDNA was
              cloned into the SalI and NotI sites of the Lambda ZIPLOX

```



REFERENCE  
AUTHORS

1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

TITLE  
JOURNAL

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

## COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

## FEATURES

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

1..18

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--02-P15"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
CDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF314452 (1-18)

Qy 49 leuArgaen 51

Db 3 CTACGTAAC 11

## RESULT 261

## CF317226/c

LOCUS CF317226 18 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--06-N14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--06-N14, mRNA sequence.  
CF317226  
ACCESSION CF317226  
VERSION CF317226.1 GI:33688987  
KEYWORDS EST.

## ORGANISM

## SOURCE

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## JOURNAL

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

## COMMENT

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--06-N14"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
CDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
CDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

## Alignment Scores:

Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF317226 (1-18)

Qy 58 GluLeuLeu 60

Db 12 GAGTGTGTG 4

## RESULT 262

## CF319738/c

LOCUS CF319738 18 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--10-P16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-P16, mRNA sequence.  
CF319738  
ACCESSION CF319738.1 GI:33691499  
VERSION CF319738.1  
KEYWORDS EST.

## ORGANISM

## SOURCE

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## ORIGIN

## Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF319738 (1-18)

QY 85 SerProCys 87

Db 16 AGTCATGT 8

## RESULT 263

## CF323060

LOCUS HDN-02-N01.g1 OSHDACL-overexpressing transgenic rice lambda phage

DEFINITION CDNA library II (HDN) Oryza sativa CDNA clone HDN-02-N01, mRNA

sequence.

ACCESSION CF323060

VERSION CF323060.1 GI:33794348

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 18  
/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HDN-02-N01"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E. coli SDR"

/clone\_lib="OSHDACL-overexpressing transgenic rice lambda

phage CDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF323060 (1-18)

QY 73 GlyArgCys 75

|||||

Db 7 GGCGGTGC 15

## RESULT 264

## CF330870/c

LOCUS NACL-06-M07.b1 Rice callus plasmid CDNA library (NACL) Oryza

DEFINITION sativa CDNA clone NACL-06-M07, mRNA sequence.

ACCESSION CF330870

VERSION CF330870.1 GI:33809964

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

Location/Qualifiers

1. 18  
/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL-06-M07"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E. coli DH10B"

/clone\_lib="Rice callus plasmid CDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## ORIGIN

## Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF330870 (1-18)

QY 85 SerProCys 87

Db 16 AGTCATGT 8

## RESULT 265

## CF332520

LOCUS JMT-01-A23.g1 AcJMT-overexpressing transgenic rice plasmid CDNA

DEFINITION library (JMT) Oryza sativa CDNA clone JMT-01-A23, mRNA sequence.

ACCESSION CF332520

VERSION CF332520.1 GI:33813259

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 18)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source 1.18  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--01-A23"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtUMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF332520 (1-18)

OY 49 LeuArgAsn 51  
|||||  
3 CTACGTAAAC 11

Db 3 CTACGTAAAC 11

RESULT 266

CF333354 18 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--02-D13.g1 AtUMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-D13, mRNA sequence.

ACCESSION CF333354  
VERSION CF333354.1 GI:33814976

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source 1.18  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--02-D13"

## ORIGIN

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF333354 (1-18)

OY 49 LeuArgAsn 51  
|||||  
3 CTACGTAAAC 11

Db 3 CTACGTAAAC 11

RESULT 267

CF334471 18 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--03-M11.g1 AtUMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-M11, mRNA sequence.

ACCESSION CF334471

VERSION CF334471.1 GI:33817267

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc., Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source 1.18  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--03-M11"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtUMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

## ORIGIN

Alignment Scores:  
Pred. No.: 3.83e+06 Length: 18  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF334471 (1-18)

QY 49 LeuArgAsn 51  
 |||||  
 3 CTACGTAC 11

RESULT 268

LOCUS D11637 18 bp mRNA linear EST 02-DEC-1992  
 DEFINITION HUM000C318 Liver HepG2 cell line. Homo sapiens cDNA clone c318,  
 mRNA sequence.  
 ACCESSION D11637  
 VERSION D11637.1 GI:2148229  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 18)  
 Okubo,K., Hori,N., Matoba,R., Niyama,T., Fukushima,A., Kojima,Y.  
 and Matsubara,K.  
 Large scale cDNA sequencing for analysis of quantitative and  
 qualitative aspects of gene expression  
 Nat. Genet. 2, 173-179 (1992)

JOURNAL MEDLINE 94258199  
 PUBMED 1345164

COMMENT Contact: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki  
 Niyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara  
 Institute for Molecular and Cellular Biology  
 Osaka University  
 1-3 Yamada-oka, Suita, Osaka 565, Japan.  
 Location/Qualifiers  
 1..18  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:D057522E"  
 /db\_xref="taxon:9606"  
 /clone="c318"  
 /lab\_host="E.coli"  
 /clone\_11b="Liver HepG2 cell line."  
 /note="T3'-directed regional cDNA library. Cleaved by MboI  
 and transformed into E.coli."

ORIGIN

Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x D11637 (1-18)

QY 31 TyrValVal 33  
 |||||  
 7 TATGTTGTG 15

RESULT 269

LOCUS L76122/c 18 bp mRNA linear EST 21-FEB-1996  
 DEFINITION SCMRAP0216 G2/KS adult worm mini-library Schistosoma mansoni cDNA  
 clone SCMRAP0216, mRNA sequence.  
 ACCESSION L76122  
 VERSION L76122.1 GI:1196860  
 KEYWORDS EST.  
 SOURCE Schistosoma mansoni  
 Schistosoma mansoni  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigeidae; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 18)  
 AUTHORS Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A., Pena,S.D. and  
 Simpson,A.U.G.  
 TITLE Multilibraries constructed from cDNA generated by arbitrarily primed  
 RT-PCR: an alternative to normalized libraries for the generation  
 of ESTs from nanogram quantities of mRNA  
 JOURNAL Gene 186 (1), 135-142 (1997)  
 MEDLINE 97199380  
 PUBMED 9047356

COMMENT Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A.,  
 Pena,S.D. and Simpson,A.U.G.  
 Location/Qualifiers  
 1..18  
 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6183"  
 /clone="SCMRAP0216"  
 /note="A mini-library was made by cloning products derived  
 from RNA-arbitrarily primed PCR (RAP PCR) profiles into  
 the pUC 18 vector. Reverse transcription of adult worm  
 mRNA was primed with G2and subsequent PCR amplification  
 was performed in the presence of primer KS"

ORIGIN

Alignment Scores:  
 Pred. No.: 3.83e+06 Length: 18  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x L76122 (1-18)

QY 185 GluValAsp 187  
 |||||  
 11 GAGGTGCAC 3

RESULT 270

ID HSM007596 standard; mRNA; EST; 19 BP.  
 ID HSM007596  
 AC AL042746;  
 SV AL042746.1

DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DB Homo sapiens mRNA; EST DKFZp434C1822\_r1 (from clone DKFZp434C1822)

KW EST; expressed sequence tag.

OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 [1]  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;  
 submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferpitz 18a D-82152 Martinsried, GERMANY  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No st sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de  
 FH Key Location/Qualifiers

```

FH source 1..19
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: hres3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;

Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x HSM007596 (1-19)

QY 131 ArgAlaGly 133
DB 1 CGCGCGCGGT 9

RESULT 271
HSM007596/c
ID HSM007596 standard; mRNA; EST; 19 BP.
XX
XX AL042746.1
XX
XX
XX 12-MAR-1999 (rel. 59, Created)
XX 12-MAR-1999 (rel. 59, Last updated, Version 1)
XX
XX Homo sapiens mRNA; EST DKFZp434C1822_r1 (from clone DKFZp434C1822)
XX
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX [1]
XX 1-19
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Kiofererspitze 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by LMU within the CDNA
XX sequencing consortium of the German Genome Project
XX No si sequence available
XX This clone is available at the RZPD in Berlin
XX Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX Key Location/Qualifiers
FH source 1..19
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: hres3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;

```

```

Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x HSM007596 (1-19)

QY 193 PheArgThr 195
DB 15 TTCGGAGCC 7

RESULT 272
AA884867/c
LOCUS AA884867
DEFINITION AA884867 19 bp mRNA linear EST 04-JAN-1999
am21d11.s1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:1467453 3' similar to TR:Q93040 Q93040 TIF1BETA ZINC FINGER
PROTEIN. [1] ; mRNA sequence.
ACCESSION AA884867
VERSION AA884867.1 GI:2994848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicagap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAG Consortium (info@image.lml.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 1216 Std Error: 0.00
Seq primer: -40m13 fwd. BT from Amersham
High quality sequence stop: 1.

FEATURES
source
1..19
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1467453"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT7T3D-Pec (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH119, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and as circles were made in
vitro. Following RNP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaído."
ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

```

US-09-966-880A-8 (1-198) x AA884867 (1-19)

QY 172 LeuserArg 174

DB 11 CTGTACGCA 3

RESULT 273  
AA903030

LOCUS AA903030 19 bp mRNA linear EST 19-MAY-1998  
DEFINITION Ok51a08.s1 NCI CGAP Le12 Homo sapiens cDNA clone IMAGE:1517462 3'

ACCESSION AA903030 similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST 1, mRNA sequence.

VERSION AA903030.1 GI:3038153

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT Contact: Robert Strausberg, Ph.D.

Unpublished (1997)

Email: cgapbs-remail.nih.gov

unknown library type

Trace considered overall poor quality

Insert Length: 714 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1.19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1517462"

/issue\_type="telomysarcoma"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Le12"

/note="Organ: soft tissue; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Site 1: Not I; Site 2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

15'-AAGTGAAGATTCGCGCGCATCTTTTCTTTTCTTTT-3',

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 4.05e+06 Length: 19

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA903030 (1-19)

QY 145 PheTYCYs 147

DB 2 TTTTATTGT 10

RESULT 274

AA918795

LOCUS AA918795 19 bp mRNA linear EST 10-JUN-1998

DEFINITION 0169c05.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534856 3'

similar to TR:Q39595 Q39599 EXTENSIN.1; contains TAR1.b2 TAR1

repetitive element 1, mRNA sequence.

ACCESSION AA918795

VERSION AA918795.1 GI:3058685

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

COMMENT Contact: Robert Strausberg, Ph.D.

Unpublished (1997)

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNLT at:

www.bio.lim.gov/bdip/image/image.html

Trace considered overall poor quality

Insert Length: 814 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1.19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1534856"

/issue\_type="DH10B"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Kid3"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer,

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT73 vector. mRNA

source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and

M. Fatima Bonaldo."

#### ORIGIN

##### Alignment Scores:

Pred. No.: 4.05e+06 Length: 19

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA918795 (1-19)

QY 23 GlyARGArg 25

DB 11 GGGAGGAGG 19

RESULT 275

AA918795/c

LOCUS AA918795/c 19 bp mRNA linear EST 10-JUN-1998

DEFINITION 0169c05.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534856 3'

similar to TR:Q39595 Q39599 EXTENSIN.1; contains TAR1.b2 TAR1

repetitive element 1, mRNA sequence.

ACCESSION AA918795

VERSION AA918795.1 GI:3058685

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 19)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL  
COMMENT

Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

## FEATURES

## Source

Trace considered overall poor quality  
Insert Length: 814 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

```
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534856"
/lab_host="VDH10B"
/clone_lib="NCI-CGAP_Kid3"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
```

## ORIGIN

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AA918795 (1-19)

QY 180 LeuLeuPro 182

DB 18 CTCCTCCCC 10

## RESULT 276

AA932041

LOCUS 19 bp mRNA linear EST 07-JUN-1998  
DEFINITION c035h05.s1 NCI CGAP LUS Homo sapiens cDNA clone IMAGE:1568217 3', similar to SW:NM\_016448 PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE

CHAIN 4 ; mRNA sequence.

ACCESSION AA932041

VERSION AA932041.1 GI:3087083

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

## FEATURES

## Source

Trace considered overall poor quality  
Insert Length: 525 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

```
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1568217"
/tissue_type="carcinoid"
/lab_host="VDH10B"
/clone_lib="NCI-CGAP_LUS"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
```

## ORIGIN

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AA932041 (1-19)

QY 103 AsnLeuSer 105

DB 10 AATTGAGT 18

## RESULT 277

AA934303/c

LOCUS 19 bp mRNA linear EST 26-MAR-1999  
DEFINITION SWOVJ3CAN12H12 Onchocerca volvulus infective larva cDNA (SAM94MW-OVL3) Onchocerca volvulus cDNA clone onch672 5' similar to TR:Q33571 Q33571 ATP5B SUBUNIT 6 ; mRNA sequence.

ACCESSION AA934303

VERSION AA934303.1 GI:3091460

KEYWORDS EST.

SOURCE Onchocerca volvulus

ORGANISM Onchocerca volvulus

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.

REFERENCE 1 (bases 1 to 19)

AUTHORS Williams, S.A., Lizotte-Maniewski, M., Laney, S., Wehng, L., Hillier, L., Allen, M., Bowles, L., Gesel, S., Joet, S., Kucaba, T., Martin, J., Stepien, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Riteer, E., Kohn, S., Underwood, K. and Marra, M.

UNPUBLISHED (1998)

COMMENT Molecular Parasitology OVL3

CONTACT: Steven A. Williams

Smith College Department of Biological Sciences

Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA

Tel: 4135833826

Fax: 4135833786

Email: [genome@smith.edu](mailto:genome@smith.edu)

The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email [genomesmith.edu](mailto:genomesmith.edu) When requesting this clone from Dr. Williams, please reference the Williams lab clone id - SMOV33CAN12H12  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

source

```
1. 19
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="onch672"
/lab_host="XLI-Blue MRF"
/clone_lib="Onchocerca volvulus infective larva cDNA (SAM64UL-OvL3)"
/note="Vector: lambda UniZap XR; Site_1: EcoR I; Site_2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by RsaE H and DNAPol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Wenhong Lu. The library is available from Dr. S.A. Williams, email genomesmith.edu."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AA934303 (1-19)

CY 60 Leuphelen 62

DB 17 CTTTITTTG 9

## RESULT 278

AI016864/C

LOCUS

DEFINITION

AI016864 19 bp mRNA linear EST 27-AUG-1998  
 ou27c11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone  
 IMAGE:1627508 3' similar to TR:Q35989 CYTOCHROME C OXIDASE  
 SUBUNIT 1 ; mRNA sequence.

ACCESSION AI016864.1 GI:3231200

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

REFERENCE

AUTHORS

TITLE

JOURNAL

Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LINT ; contact the  
 IMAG Consortium ([info@image.jnl.gov](mailto:info@image.jnl.gov)) for further information.  
 Trace considered overall poor quality  
 Insert Length: 358 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

COMMENT

FEATURES

source

```
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

```
/clone="IMAGE:1627508"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  

a modified polylinker; Site_1: Not I; Site_2: Eco RI;  

Equal amounts of plasmid DNA from three normalized  

libraries (fetal lung NBH119W, testis NHT, and B-cell  

NCI CGAP GCBI) were mixed, and ss circles were made in  

vitro. Following HAP purification, this DNA was used as  

tracer in a subtractive hybridization reaction. The driver  

was PCR-amplified cDNAs from pools of 5,000 clones made  

from the same 3 libraries. The pools consisted of  

I.M.A.G.E. clones 297480-302087, 682632-687239,  

726408-728711, and 729096-731399. Subtraction by Bento  

Soares and M. Fatima Bonaldo."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AI016864 (1-19)

CY 83 SerTpsr 85

DB 15 TCTGTCTT 7

## RESULT 279

AI017940

LOCUS

DEFINITION

AI017940 19 bp mRNA linear EST 27-AUG-1998  
 ou24b04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone  
 IMAGE:1627183 3' similar to SW:ME4C DROME O01644 MALE SPECIFIC  
 SPERM PROTEIN MST84DC. ; contains TAA1.t3 TAA1 repetitive element ;  
 mRNA sequence.

ACCESSION AI017940

VERSION AI017940.1 GI:3232276

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

REFERENCE

AUTHORS

TITLE

JOURNAL

Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 This clone is available royalty-free through LINT ; contact the  
 IMAG Consortium ([info@image.jnl.gov](mailto:info@image.jnl.gov)) for further information.  
 Trace considered overall poor quality  
 Insert Length: 1853 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

COMMENT

FEATURES

source

```
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1627183"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  

a modified polylinker; Site_1: Not I; Site_2: Eco RI;  

Equal amounts of plasmid DNA from three normalized  

libraries (fetal lung NBH119W, testis NHT, and B-cell  

NCI CGAP GCBI) were mixed, and ss circles were made in  

vitro. Following HAP purification, this DNA was used as  

tracer in a subtractive hybridization reaction. The driver
```

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A107581 (1-19)

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
4.05e+06	3.00	100.00%	100.00%	1.52%	9
Length: 19	Matches: 3	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0

US-09-966-880A-8 (1-198) x A107581 (1-19)

QY 118 Asparglys 120

Db 1 GACCGGAAA 9

## RESULT 280

A1077581

## LOCUS

oy26a04.s1 Soares senescent fibroblasts NBHSF Homo sapiens CDNA

## DEFINITION

clone IMAGE:166526 3' similar to SW:PP1 HUMAN P48556 26S  
PROTEASOME REGULATORY SUBUNIT P31. ; mRNA sequence.

ACCESSION A1077581

VERSION A1077581.1 GI:3411989

## KEYWORDS

EST. Homo sapiens (human)

## SOURCE

Organism Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 19)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

## AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: cgaps-remail.nih.gov  
This clone is available royally-free through LINT; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Trace considered overall poor quality  
Insert Length: 897 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

## source

```
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:166526"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts NBHSF"
/notes="Vector: pRTT3D (Pharmacia) with a modified
polylinker V-type; phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:
4.05e+06	3.00	100.00%

Length:	Matches:	Conservative:
19	3	0

US-09-966-880A-8 (1-198) x A107581 (1-19)

QY 195 Thrleugly 197

Db 4 ACACTGGGT 12

## RESULT 281

A1078728

## LOCUS

oy12i07.s1 Soares senescent fibroblasts NBHSF Homo sapiens CDNA

## DEFINITION

clone IMAGE:166537 3' similar to SW:POR2 HUMAN P45880  
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2 ; mRNA  
sequence.

ACCESSION A1078728

VERSION A1078728.1 GI:3411650

## KEYWORDS

EST. Homo sapiens (human)

## SOURCE

Organism Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 19)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

## AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

## JOURNAL

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: cgaps-remail.nih.gov  
This clone is available royally-free through LINT; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.

## FEATURES

Trace considered overall poor quality  
Insert Length: 575 Std Error: 0.00  
Seq primer: -40m3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

## source

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1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:166537"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts NBHSF"
/notes="Vector: pRTT3D (Pharmacia) with a modified
polylinker V-type; phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."
```

## ORIGIN

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
4.05e+06	3.00	100.00%	100.00%	1.52%	9
Length: 19	Matches: 3	Conservative: 0	Mismatches: 0	Indels: 0	Gaps: 0

US-09-966-880A-8 (1-198) x A1078728 (1-19)

QY 104 Leuserleu 106

Db 6 TTAAAGCTC 14

RESULT 282  
A1147066/c  
LOCUS A1147066 19 bp mRNA linear EST 29-SEP-1998  
DEFINITION CK3b08.s1 Soares NSF P8 9W OT PA P S1 Homo sapiens cDNA clone IMAGE:1509591.3' similar to TR:O05039 009039 LINKER OF T-CELL RECEPTOR PATHWAYS ; contains TARI.t2 TARI repetitive element ;, mRNA sequence.

ACCESSION A1147066 GI:3674748  
VERSION A1147066  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 1.

FEATURES  
Source  
1..19  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1509591"  
/lab\_host="DH10B"  
/clone\_lib="Soares NSF P8 9W OT PA P S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HP pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1147066 (1-19)

QY 171 ArgLeuser 173  
Db 12 AGGTTGCA 4

RESULT 283  
A1155325  
LOCUS A1155325 19 bp mRNA linear EST 30-SEP-1998  
DEFINITION ud88a05.r1 Soares NMPu Mus musculus cDNA clone IMAGE:1477904.5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;, mRNA sequence.

ACCESSION A1155325

VERSION A1155325.1 GI:3683794  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Maria M., Hillier L., Allen M., Bowles M., Dietrich N., Dubuque T., Geisler S., Kucaba T., Lacy M., Le M., Martin J., Morris M., Scheinberg K., Steptoe M., Tan F., Underwood K., Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R. and Waterston R.  
TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
WGI:926260  
Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 RT from Amersham  
High quality sequence stop: 1.

FEATURES  
Source  
1..19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1477904"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Soares NMPu"  
/note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Alignment Scores:  
Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1155325 (1-19)

QY 172 LeuserArg 174  
Db 4 CTATCTGCA 12

RESULT 284  
A1360784/c  
LOCUS A1360784 19 bp mRNA linear EST 15-FEB-1999  
DEFINITION GR98G07.r1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2010588.3' similar to TR:Q41107 Q41107 EXTENSIN CLASS 1 PROTEIN PRECURSOR ;, mRNA sequence.

ACCESSION A1360784  
VERSION A1360784.1 GI:4112405  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 19)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BRGAP), Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bdrp/image/image.html](http://www.bio.lnl.gov/bdrp/image/image.html)  
Insert Length: 973 Std Error: 0.00  
Seq primer: -40UP from G1bco  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

## source

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1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2010588"
/tissue_type="Glioblastoma (pooled)"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Brn23"
/notes="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCGCATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
```

## ORIGIN

Alignment Scores:  
Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x A1360784 (1-19)

QY 131 ArgAlaGly 133  
Db 17 AGGGCAGGG 9  
RESULT 285  
A1371092  
LOCUS  
DEFINITION  
A1371092 19 bp mRNA linear EST 16-FEB-1999  
ta07909.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2043424 3'  
similar to TR:Q26195 Q26195 PVAL GENE, contains 11.b3 L1  
repetitive element ;, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
A1371092.1 GI:4149845  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 19)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project

JOURNAL  
COMMENT  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bdrp/image/image.html](http://www.bio.lnl.gov/bdrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 536 Std Error: 0.00  
Seq primer: -40UP from G1bco  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

## source

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1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2043424"
/tissue_type="Glioblastoma (pooled)"
/lab_host="DH10B"
/clone_1ib="NCI CGAP Brn23"
/notes="Organ: Brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGGCGCATATCTTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."
```

## ORIGIN

Alignment Scores:  
Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: Gaps: 0

US-09-966-880A-8 (1-198) x A1371092 (1-19)

QY 42 PheSerLeu 44  
Db 9 TTTTCTCTT 17  
RESULT 286  
A1431460  
LOCUS  
DEFINITION  
A1431460 19 bp mRNA linear EST 13-APR-1999  
th40c01.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2120736 3'  
similar to TR:Q04117 Q04117 SALIVARY PROLINE-RICH PROTEIN RP4  
PBCURSOR, contains element WSKI repetitive element ;, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
A1431460.1 GI:4303341  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 19)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb-remail.nih.gov](mailto:cgapsb-remail.nih.gov)

Life Technologies catalog #: 11547-015  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLNI at:  
[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 653 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2120736"  
 /tissue\_type="lymphoma, follicular mixed small and large  
 cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Lym12"  
 /note="Organ: lymph node; Vector: PCMV-SPORT6; Site 1:  
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:  
 Oligo dt. Average insert size 1.25 kb. Life Technologies  
 catalog #: 11547-015"

/mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2134162"  
 /tissue\_type="lymphoma, follicular mixed small and large  
 cell"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI-CGAP Lym12"  
 /note="Organ: lymph node; Vector: PCMV-SPORT6; Site 1:  
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:  
 Oligo dt. Average insert size 1.25 kb. Life Technologies  
 catalog #: 11547-015"

## ORIGIN

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1431460 (1-19)

QY 130 Hsargala 132

Db 3 CACAGGCC 11

RESULT 287

A1433480

LOCUS A1433480 19 bp mRNA linear EST 30-MAR-1999

DEFINITION t153a06.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134162 3'

similar to SW:BRPp HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E

; contains element TARI repetitive element ; mRNA sequence.

ACCESSION A1433480

VERSION A1433480.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 19)

JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLNI at:

[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1003 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1..19

/organism="Homo sapiens"

Alignment Scores:  
 Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1433480 (1-19)

QY 72 Proglyarg 74

Db 10 CCGGCGCGC 18

RESULT 288

A1524591/c

LOCUS A1524591 19 bp mRNA linear EST 12-MAY-1999

DEFINITION t043f09.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2181833 3'

similar to SW:NU4M PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE

CHAIN 4 ; mRNA sequence.

ACCESSION A1524591

VERSION A1524591.1

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE 1 (bases 1 to 19)

JOURNAL NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/BLNI at:

[www.bio.lnl.gov/bbrp/image/image.html](http://www.bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 502 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLVA=No. Location/Qualifiers

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2181833"

/tissue\_type="serous papillary carcinoma, high grade, 2

pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP U4"

/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

ORIGIN Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) X A1524591 (1-19)

QY 156 GUAAGTTH 158  
DB 19 GACGCACT 11

## RESULT 289

A1538541/c 19 bp mRNA linear EST 13-APR-1999  
LOCUS t008a1.x1 NCI CGAP CLU1 Homo sapiens cDNA clone IMAGE:2075036 3'  
DEFINITION similar to TR:Q60843 Q60843 LUNG KRUPPEL-LIKE FACTOR ;, mRNA  
sequence.

ACCESSION A1538541 GI:4452676  
VERSION A1538541  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 19)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Unpublished (1997)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
www.bio.lml.gov/bbrp/image/image.html

## JOURNAL

## COMMENT

Trace considered overall poor quality  
Insert Length: 497 Std Error: 0.00  
Seg primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

## FEATURES

## source

1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2075036"  
/tissue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="NCI CGAP CLU1"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTACCAATCTGAAGTGGAGCGCGCATGTCTTTTCTTTTCTTTTCTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
library is normalized, and was constructed by Bento  
Soares and M.Fatima Bernaldo."

ORIGIN Alignment Scores:  
Pred. No.: 4.05e+06 Length: 19

Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) X A1538541 (1-19)

QY 132 AAGIYVAI 134  
DB 13 GCAAGTGTG 5

## RESULT 290

A1583857 19 bp mRNA linear EST 14-DEC-1999  
LOCUS t173g05.x1 NCI CGAP HSC3 Homo sapiens cDNA clone IMAGE:2246456 3'  
DEFINITION similar to SW:RL37\_HUMAN P02403 60S RIBOSOMAL PROTEIN L37 ;, mRNA  
sequence.

ACCESSION A1583857 GI:4569754  
VERSION A1583857.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.  
AUTHORS 1 (bases 1 to 19)  
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Unpublished (1997)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,  
M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
www.bio.lml.gov/bbrp/image/image.html

## JOURNAL

## COMMENT

Trace considered overall poor quality  
Insert Length: 472 Std Error: 0.00  
Seg primer: -40UP from Gibco  
High quality sequence stop: 1  
Location/Qualifiers

## FEATURES

## source

1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2246456"  
/tissue\_type="CD34+, T negative, patient with chronic  
myelogenous leukemia"  
/lab\_host="DH10B"  
/clone.lib="NCI CGAP HSC3"  
/note="Organ: bone marrow; Vector: pAMP1, mRNA made from  
lymphoid tissue, cDNA made by oligo-dT priming.  
directionally cloned. Size-selected on agarose gel,  
average insert size 500 bp. Primary library,  
non-amplified. cDNA library Preparation: David B.  
Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer  
Research 56:5380-5385."

## ORIGIN Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
Score: 3.00 Matches: 3  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 1.52% Indels: 0  
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1583857 (1-19)

QY 139 MetThrphe 141  
 |||||  
 11 ATGACGTC 3

RESULT 291  
 A1584018 19 bp mRNA linear EST 14-DEC-1999  
 LOCUS ts12e10.x1 NCI\_CGAP\_Panl Homo sapiens cDNA clone IMAGE:2228394 3'  
 DEFINITION similar to SW:FRPL\_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO ;,  
 mRNA sequence.

ACCESSION A1584018  
 VERSION A1584018.1 GI:4569915  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Life Technologies catalog #: 11548-013  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbtp/image/image.html

FEATURES  
 source Location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2228394"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Panl"  
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x A1584018 (1-19)

QY 72 ProglyArg 74  
 |||||  
 8 CCGGCGCC 16

RESULT 292  
 A1597783 19 bp mRNA linear EST 14-MAY-1999  
 LOCUS tr12g04.x1 NCI\_CGAP\_Panl Homo sapiens cDNA clone IMAGE:2228582 3'  
 DEFINITION similar to SW:DDX3\_MOUSE Q62167 DEAD BOX PROTEIN 3 ;, mRNA  
 sequence.

ACCESSION A1597783  
 VERSION A1597783

VERSION A1597783.1 GI:4606831  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Life Technologies catalog #: 11548-013  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www.bio.llnl.gov/bbtp/image/image.html  
 Insert Length: 842 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1  
 POLYA-No.

FEATURES  
 source Location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2226582"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP\_Panl"  
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x A1597783 (1-19)

QY 39 AlaThrSer 41  
 |||||  
 11 GCCACCTCC 19

RESULT 293  
 A1664013 19 bp mRNA linear EST 10-MAY-1999  
 LOCUS ue7a11.r1 Scores NMPu Mus musculus cDNA clone IMAGE:1496732 5'  
 DEFINITION similar to TR:O89050 O89050 MUSKELIN. ;, mRNA sequence.

ACCESSION A1664013  
 VERSION A1664013.1 GI:4767596  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 NCI\_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:934336

Trace considered overall poor quality  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

1..19

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1496732"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

/clone\_lib="Soares\_NMPu"  
 /note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1664013 (1-19)

QY 35 ArgArgasp 37

Db 1 AGAAGAGAC 9

RESULT 294  
A1664013/c

LOCUS A1664013 19 bp mRNA linear EST 10-MAY-1999  
 DEFINITION ue73a11.x1 Soares NMPu Mus musculus cDNA clone IMAGE:1496732 5'  
 similar to TR:089050 089050 MUSKELIN. ; mRNA sequence.

ACCESSION A1664013  
 VERSION A1664013.1 GI:4767596  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through JLNLI; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:934336

## FEATURES

1..19

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1496732"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"

## ORIGIN

/clone\_lib="Soares\_NMPu"  
 /note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

## Alignment Scores:

Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1664013 (1-19)

QY 104 LeuSerLeu 106

Db 11 TTGTCTCTT 3

RESULT 295  
A1747751/c

LOCUS A1747751 19 bp mRNA linear EST 22-JUN-1999  
 DEFINITION u121h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone  
 IMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND  
 POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ; mRNA sequence.

ACCESSION A1747751  
 VERSION A1747751.1 GI:5126015  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
 Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,  
 Ritter, E., Koh, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
 Waterston, R. and Wilson, R.  
 The WashU-NCI Mouse EST Project 1999  
 Unpublished (1999)  
 CONTACT: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through JLNLI; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:995933

JOURNAL Unpublished (1999)  
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through JLNLI; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:995933

## FEATURES

1..19

/organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:2088249"  
 /dev\_stage="embryo, 14 dpc"  
 /lab\_host="DH10B"  
 /clone\_lib="Sugano mouse embryo mewa"  
 /note="Vector: pWE18S-FL3; Site 1: DraIII (CAAGTGTG);  
 Site 2: DraIII (CAAGTGTG); 1st strand cDNA was primed  
 with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];  
 double-stranded cDNA was ligated to a DraIII adaptor

## ORIGIN

[TGTGTGCTACTG], digested and cloned into distinct DraIII sites of the pWE18S-PL3 vector (5' site CACGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1747751 (1-19)

OY 104 LeuSerLeu 106  
 DB 11 CTCTCCTG 3

RESULT 296  
 A1758301 19 bp mRNA linear EST 16-DEC-1999  
 LOCUS A1758301/c ty06a07.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278260 3'  
 DEFINITION similar to SW:SP49 HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49  
 ;contains MSRI.b2 MSRI repetitive element //, mRNA sequence.

ACCESSION A1758301 GI:5152024  
 VERSION A1758301  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLMT at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 1803 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

## FEATURES

location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2278260"  
 /tissue\_type="poorly-differentiated endometrial  
 adenocarcinoma, 2 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut3"  
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.45 kb. Life Technologies catalog #:  
 11541-018"

ORIGIN

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1758301 (1-19)

OY 23 G1ArgArg 25  
 DB 13 GCGAGCGCG 5

RESULT 297  
 A1811474 19 bp mRNA linear EST 15-DEC-1999  
 LOCUS A1811474 tw43c04.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2262438 3'  
 DEFINITION similar to TR:O61645 O61649 PYROLIDONE-RICH ANTIGEN. ;contains  
 element MSRI repetitive element //, mRNA sequence.

ACCESSION A1811474 GI:5398040  
 VERSION A1811474  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 19)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/BLMT at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 1729 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2262438"  
 /tissue\_type="well-differentiated endometrial  
 adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut1"  
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

## FEATURES

source

## ORIGIN

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1811474 (1-19)

CY 23 GATGATG 25  
 DB 5 GGGAGGCG 13  
 RESULT 298  
 A1918188 19 bp mRNA linear EST 13-DEC-1999  
 A1918188/c  
 LOCUS tno8609.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167024 3'  
 DEFINITION similar to TR:089051 089051 E253 PROTEIN. mRNA sequence.  
 ACCESSION A1918188  
 VERSION A1918188.1 GI:5638043  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BrTGP), Tumor Gene Index  
 COMMENT Unpublished (1998)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgaps-rc@mail.nih.gov  
 COMMENT Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/ILMN at:  
 www.bio.lln.gov/bdrp/image/image.html  
 Insert Length: 1154 Std Error: 0.00  
 Seq primer: -40UP from G1bco  
 High quality sequence stop: 1.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2167024"  
 /issue\_type="anaplastic oligodendroglioma"  
 /lab\_host="DH10B"  
 /clone\_1lb="NCI CGAP Brn25"  
 /note="Organ: Brain; Vector: pTT3D-Pac (Pharmacia) with a  
 modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCGCATGATGTTTTTTTTTTTTTTT  
 T 3']: double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pTT3D vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M.Fatima Bonaldo."  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-966-880a-8 (1-198) x A1918188 (1-19)  
 CY 30 CysTyrVal 32  
 DB 16 TGTATGTG 8  
 RESULT 299  
 A0061154

LOCUS A0061154 19 bp mRNA linear EST 20-MAY-1999  
 DEFINITION A0061154 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium  
 discoideum cDNA clone SLD408, mRNA sequence.  
 ACCESSION A0061154  
 VERSION A0061154.1 GI:4882258  
 KEYWORDS EST.  
 SOURCE Dictyostelium discoideum  
 ORGANISM Dictyostelium discoideum  
 Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,  
 Yoshino,R., Mitsu,B.N., Pi,M., Saito,T., Takemoto,K., Yasukawa,H.,  
 Williams,D., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.  
 TITLE Developmental cDNA in Dictyostelium discoideum  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Hideko Urushihara  
 Institute of Biological Sciences  
 University of Tsukuba  
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
 Tel: 81-298-53-4664  
 Fax: 81-298-53-6614  
 Email: hidekobiol.tsukuba.ac.jp  
 PROJECT = Dictyostelium discoideum cDNA project in Japan.  
 Location/Qualifiers  
 1..19  
 /organism="Dictyostelium discoideum"  
 /mol\_type="mRNA"  
 /strain="AX4"  
 /db\_xref="taxon:44689"  
 /clone="SLD408"  
 /dev\_stage="slug"  
 /clone\_1lb="Dictyostelium discoideum SL (H.Urushihara)"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 4.05e+06 Length: 19  
 Score: 3.00 Matches: 3  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 1.52% Indels: 0  
 DB: 9 Gaps: 0  
 US-09-966-880a-8 (1-198) x A0061154 (1-19)  
 CY 74 ArgCysTyr 76  
 DB 4 AGATGTTAT 12  
 RESULT 300  
 A0059909 19 bp mRNA linear EST 23-AUG-2000  
 LOCUS A0059909  
 DEFINITION A0059909 best.upc15.ba.A040e11 UPC15 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION A0059909  
 VERSION A0059909.1 GI:6652231  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 19)  
 AUTHORS Brenner,S., Williams,S.R., Vermaas,B.H., Storck,T., Moon,K.,  
 McCoilum,C., Mao,J.I., Kirchner,D.J., Ellett,S., Dubridge,R.B.,  
 Burcham,T. and Albrecht,G.  
 TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical  
 separation of differentially expressed cDNAs  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)  
 MEDLINE 20144098  
 PUBMED 10677516  
 COMMENT Contact: Burcham TS  
 LYNX Therapeutics, Inc.  
 25861 Industrial Blvd., Hayward, CA 94545, USA  
 Tel: 510 670 9338  
 Fax: 510 670 9302

Email: timb@lynxgen.com  
Sequence obtained from LYNX Therapeutics Megascort technology.  
Collected from the up-regulated gate.  
High quality sequence stop: 19.  
Location/Qualifiers

## FEATURES

source 1. 19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/cell\_type="monocytic leukemia"  
/cell\_line="THP-1 (TIB-202)"  
/clone\_id="UPC15"  
/note="Vector: pCR2.1; Cloning of PCR products from  
micro-beads carrying 3' end of up-regulated cDNA. THP-1  
cells induced with 100 nM PMA in DMSO. "

## ORIGIN

## Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880a-8 (1-198) x AM059909 (1-19)

QY 195 ThrLeuGly 197

Db 3 ACTTGGGA 11

Search completed: March 5, 2004, 02:19:27  
Job time : 2522 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 20:57:37 ; Search time 360 Seconds  
(without alignments)  
7044.928 Million cell updates/sec

Title: US-09-966-880a-7\_COPY\_80\_676  
Perfect score: 597  
Sequence: 1 atggacagcgccttgatgaa.....ttcgactctggacttga 597

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1690386

Minimum DB seq length: 0  
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

1: geneeqn1980s:\*  
2: geneeqn1990s:\*  
3: geneeqn2000s:\*  
4: geneeqn2001as:\*  
5: geneeqn2001bs:\*  
6: geneeqn2002s:\*  
7: geneeqn2003as:\*  
8: geneeqn2003bs:\*  
9: geneeqn2003cs:\*  
10: geneeqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	2.5	17	2	AAA20708 Integrin
2	15	2.5	20	3	AA275674 Human b1a
3	14	2.3	16	3	AA13058 Antisense
4	14	2.3	17	2	AAA20709 Integrin
5	14	2.3	17	9	AB234570 Tumour su
6	14	2.3	17	9	ADB24297 Tumour su
7	14	2.3	20	2	AAV09174 Phospho
8	14	2.3	20	2	AAV09175 Phospho
9	14	2.3	20	6	AB230588 Candida a
10	14	2.3	20	7	ACA90226 Novel hum
11	14	2.3	20	9	ADC26512 NOV prote
12	13	2.2	17	6	AB234574 Glycosat
13	13	2.2	17	6	AB234574 Glycosat
14	13	2.2	17	6	AB234574 Glycosat
15	13	2.2	17	6	AB234574 Glycosat
16	13	2.2	17	6	AB234574 Glycosat
17	13	2.2	17	6	AB234574 Glycosat
18	13	2.2	17	6	AB234574 Glycosat
19	13	2.2	17	6	AB234574 Glycosat
20	13	2.2	17	6	AB234574 Glycosat
21	13	2.2	17	6	AB234574 Glycosat
22	13	2.2	17	6	AB234574 Glycosat
23	13	2.2	17	6	AB234574 Glycosat

C 24	13	2.2	17	7	ADA99327	ADA99327 Human MDZ
C 25	13	2.2	17	7	ADA99328	ADA99328 Human MDZ
C 26	13	2.2	17	7	ADA99328	ADA99328 Human MDZ
C 27	13	2.2	17	7	AB261946	AB261946 Human H-R
C 28	13	2.2	17	7	AB261946	AB261946 Human H-R
C 29	13	2.2	18	3	AA244774	AA244774 Human FAD
C 30	13	2.2	19	2	AA244774	AA244774 Human FAD
C 31	13	2.2	19	3	AAA83045	AAA83045 cdk6 ribo
C 32	13	2.2	19	3	AAA83046	AAA83046 cdk6 ribo
C 33	13	2.2	19	3	AAA83046	AAA83046 cdk6 ribo
C 34	13	2.2	19	5	AAH58207	AAH58207 Cell-cycl
C 35	13	2.2	19	5	AAH58208	AAH58208 Cell-cycl
C 36	13	2.2	19	7	ACR03639	ACR03639 Human NOV
C 37	13	2.2	20	2	AAQ71065	AAQ71065 Primer #1
C 38	13	2.2	20	2	AAQ71065	AAQ71065 Primer #1
C 39	13	2.2	20	2	AAQ71065	AAQ71065 Primer #1
C 40	13	2.2	20	2	AAQ71065	AAQ71065 Primer #1
C 41	13	2.2	20	3	AAQ71065	AAQ71065 Primer #1
C 42	13	2.2	20	3	AAQ71065	AAQ71065 Primer #1
C 43	13	2.2	20	3	AAQ71065	AAQ71065 Primer #1
C 44	13	2.2	20	4	AAQ71065	AAQ71065 Primer #1
C 45	13	2.2	20	5	AAQ71065	AAQ71065 Primer #1

#### ALIGNMENTS

RESULT 1  
ID AAA20708 standard; RNA, 17 BP.  
AC AAA20708;  
DT 19-JUN-2000 (first entry)  
XX  
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3934.  
XX  
XX Human, aryl hydrolase nuclear transport; ARNT, TIE-2; angiogenesis;  
XX Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
XX hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;  
XX ophthalmologic; anti-inflammatory; antiarthritic; antipneumonia; ARMD;  
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
XX age related macular degeneration; inflammation; neovascular glaucoma;  
XX myopic degeneration; psoriasis; verruca vulgaris; angiodioma;  
XX tuberous sclerosis; pot-wine stain; Sturge Weber syndrome;  
XX Kippel-Trenunay-Weber syndrome; Oler-Weber-Rendu syndrome; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9950403-A2.  
XX  
XX 07-OCT-1999.  
XX  
XX 24-MAR-1999; 99MO-US006507.  
XX  
XX 27-MAR-1998; 98US-0079678P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;  
XX WPI, 1999-591315/50.  
XX  
XX Novel ribozymes for modulating the synthesis, expression and/or stability  
XX of an mRNA encoding an angiogenic factor.  
XX  
XX Claim 55; Page 162; 305pp; English.  
XX  
XX The present invention describes enzymatic nucleic acid molecules with RNA  
XX cleaving activity, which specifically cleave RNA encoded by an aryl  
XX hydrolase nuclear transporter (ARNT) gene, an integrin subunit beta 3  
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA16775 to  
XX AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,

CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their  
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to  
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086  
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;  
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and  
 CC AAA21689 to AAA22475 and AAA23253 to AAA23342 represent ribozyme sequences  
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to  
 CC AAA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT.  
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related  
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiodioma of tuberous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kippel-Treunmayer-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 CC  
 CC Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 2.5%; Score 15; DB 2; Length 17;  
 Best Local Similarity 73.3%; Pred. No. 3.7e+03;  
 Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 36 TTACCAATTCAAAA 50  
 Db 1 UUAACAATTCAAAA 15

RESULT 2  
 AAZ75674/c  
 AAZ75674 standard; DNA; 20 BP.

AC AAZ75674;  
 XX  
 DT 10-SEP-2001 (first entry)  
 XX

DE Human biallelic marker downstream amplification primer SEQ ID NO:10030.

KW Human genome; biallelic marker; high density disequilibrium map;  
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;  
 KW haplotyping; hybridisation; identification; characterisation;  
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KW diagnosis; ss.

OS Homo sapiens.

PN WO954500-A2.

XX  
 PD 28-OCT-1999.

PF 21-APR-1999; 99WO-IB000822.

XX  
 PR 21-APR-1998; 98US-0082614P.

PR 23-NOV-1998; 98US-0109732P.

PA (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX  
 DR WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.

XX Claim 8; Page 2369; 2745pp; English.

CC AAZ6654 to AAZ69578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention

XX Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.5%; Score 15; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 GAGCAAGTTCTTTA 38  
 Db 15 GAGCAAGTTCTTTA 1

RESULT 3  
 AAA13058/c  
 ID AAA13058 standard; DNA; 16 BP.

XX  
 AC AAA13058;

DT 14-JUL-2000 (first entry)

DE Antisense oligonucleotide #16 targeting the PTS operon.

XX Antisense oligonucleotide; treat; inhibit translation; diagnose;

KW cell wall biosynthesis; ribosomal RNA; ribosomal protein; pathogenicity;

KW nutrient uptake; bacterial infection; PTS operon; Haemophilus influenzae;

KW phosphoenolpyruvate-sugar phosphotransferase system; ss.

XX Haemophilus influenzae.

PN WO200015265-A1.

XX 23-MAR-2000.

PF 15-SEP-1999; 99WO-US021950.

XX 16-SEP-1998; 98US-0100591P.

PR 16-SEP-1998; 98US-0100598P.

PR 16-SEP-1998; 98US-0100599P.

XX 16-SEP-1998; 98US-0100625P.

XX (VITA-) VITAGENIX INC.

XX Selfert W;

XX WPI; 2000-271267/23.

XX New antisense oligonucleotide, useful for treating and diagnosing  
 PT bacterial infections, interacts with and inhibits translation of a target  
 PT RNA sequence in bacteria.

XX Claim 10; Page 29; 50pp; English.

CC This sequence represents an antisense oligonucleotide that targets genes  
 CC of the phosphoenolpyruvate-sugar phosphotransferase system (PTS) operon.  
 CC The invention relates to antisense oligonucleotides (e.g. the present  
 CC sequence) which interact with and inhibit translation of a target RNA  
 CC sequence in a bacterium. The RNA sequences that the oligonucleotides  
 CC target encode proteins such as enzymes for biosynthesis of cell wall  
 CC proteins, ribosomal RNA, ribosomal proteins, proteins essential for  
 CC nutrient uptake, proteins associated with pathogenicity, subunits of DNA-  
 CC dependent RNA polymerase, and DNA polymerase. The antisense

CC oligonucleotides are used to treat or diagnose bacterial infections  
 XX Sequence 16 BP; 4 A; 3 C; 4 G; 5 T; 0 U; 0 Other;  
 SQ

Query Match 2.3%; Score 14; DB 3; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 GACCTTCAAGATT 430  
 |||||  
 Db 16 GACCTTCAAGATT 3

RESULT 4  
 AAA20709  
 ID AAA20709 standard; RNA; 17 BP.  
 XX  
 AC AAA20709;  
 XX  
 DT 19-JUN-2000 (first entry)  
 XX  
 DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3935.  
 XX  
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;  
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;  
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;  
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; AMD;  
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;  
 KW age related macular degeneration; inflammation; neovascular glaucoma;  
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;  
 KW tubercous sclerosis; pot-wine stain; Sturge Weber syndrome;  
 KW Kipfel-Trenauay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9950403-A2.  
 XX  
 PD 07-OCT-1999.  
 XX  
 PF 24-MAR-1999; 99WO-US006507.  
 XX  
 PR 27-MAR-1998; 98US-0079678P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA.  
 XX  
 DR WPI; 1999-591315/50.  
 XX  
 PT Novel ribozymes for modulating the synthesis, expression and/or stability  
 PT of an mRNA encoding an angiogenic factors.  
 XX  
 PS Claim 55; Page 162; 305pp; English.  
 XX  
 CC The present invention describes enzymatic nucleic acid molecules with RNA  
 CC cleaving activity, which specifically cleave RNA encoded by an aryl  
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3  
 CC gene, an integrin alpha 6 subunit gene, or a TIE-2 gene. AA16775 to  
 CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,  
 CC and AA17168 to AA17560 and AA17623 to AA17684 represent their  
 CC corresponding target sequences. AA17685 to AA18385 and AA19087 to  
 CC AA19154 represent ribozyme sequences for TIE-2, and AA18386 to AA19086  
 CC and AA19155 to AA19222 represent their corresponding target sequences;  
 CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme  
 CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and  
 CC AA21596 to AA21688 represent their corresponding target sequences;  
 CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence  
 CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to  
 CC AA23422 represent their corresponding target sequences. The ribozymes of  
 CC the invention are used for modulating the synthesis, expression and/or  
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,  
 CC integrin subunit beta-3, integrin subunit alpha-6, or TIE-2. They are  
 CC especially used to treat cancer, diabetic retinopathy, age related

CC macular degeneration (AMD), inflammation, and arthritis, as well as  
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,  
 CC angiofibroma of tubercous sclerosis, pot-wine stains, Sturge Weber  
 CC syndrome, Kipfel-Trenauay-Weber syndrome, Osler-Weber-Rendu syndrome,  
 CC and other syndromes and diseases related to the levels of ARNT, TIE-2,  
 CC integrin subunit alpha-6, or integrin subunit beta-3  
 XX

Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;  
 SQ

Query Match 2.3%; Score 14; DB 2; Length 17;  
 Best Local Similarity 78.6%; Pred. No. 1.2e+04;  
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 37 TACCAATTCAAAA 50  
 :|||:|  
 Db 1 UACCAATUCAAAA 14

RESULT 5  
 ABT34570  
 ID ABT34570 standard; DNA; 17 BP.  
 XX  
 AC ABT34570;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID No 207.  
 XX  
 KW Cytostatic; vinuclide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KW schizoprenia; protein chip; gene therapy; tumour suppression;  
 KW human fukutin; ds.  
 KW  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025175-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-1B004208.  
 XX  
 PR 17-SEP-2001; 2001PR-00011978.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Teletman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 58; 720pp; French.  
 XX  
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterised by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizoprenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and

CC both the polypeptide and antibodies are useful as components of protein  
CC chips. The nucleic acid sequences of the invention can be used in gene  
CC therapy. This polynucleotide sequence represents a tumour suppression  
CC related human fukutin oligonucleotide of the invention  
XX  
SQ Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 2.3%; Score 14; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 247 TCCTGGAGCCCTG 260  
DB 3 TCCTGGAGCCCTG 16  
RESULT 6  
ADB42497  
ID ADB42497 standard; DNA; 17 BP.  
XX  
AC ADB42497;  
XX  
DT 18-DEC-2003 (revised)  
DT 04-DEC-2003 (first entry)  
XX  
DE Tumour suppression/reversion associated nucleotide #2820.  
XX  
KM cytostatic; antiviral; neuroprotective; nocitropic; neuroleptic; ss;  
KM primer; probe; tumour suppression; tumour reversion; apoptosis;  
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
KM diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN MO2003040369-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 17-SEP-2002; 2002MO-1B004219.  
XX  
PR 17-SEP-2001; 2001FR-00011981.  
XX  
PA (MOLE-) MOLECULAR ENGINES LAB.  
XX  
PI Teletman A, Amson R, Twijnder M;  
DR WPI; 2003-441574/41.  
XX  
PT New nucleic acid encoding human prostate membrane-specific antigen.  
PT useful e.g. for treatment of tumors and viral infection, also related  
PT polypeptide and antibodies.  
XX  
PS Disclosure; Page 361; 771pp; French.  
XX  
XX The invention relates to the isolation of 6327 nucleotide sequences.  
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
CC sequence having at least 80% identity after optimal alignment, with the  
CC nucleotides, a sequence that hybridizes under stringent conditions with  
CC the nucleotides, or the complement, or corresponding RNA, of the  
CC nucleotides. The nucleotides are used as probes or primers for detecting,  
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
CC sense and antisense sequences, of nucleotides involved in tumour  
CC suppression or reversion, apoptosis and or viral resistance, to produce  
CC recombinant polypeptides, and to prepare transgenic animals, as  
CC experimental models. The nucleotides (also vectors containing them and  
CC cells containing the vectors), the encoded polypeptides and antibodies  
CC (Ab) against the polypeptide are useful for prevention and/or treatment  
CC of viral infections or diseases characterized by development of tumours  
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
CC Analysis of the expression of the nucleotides can be used for diagnosis  
CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
CC also be used to screen for their specific interactive molecules,  
CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.  
XX  
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.3%; Score 14; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 422 TCAAGATTATTT 435  
DB 3 TCAAGATTATTT 16  
RESULT 7  
AAV09174  
ID AAV09174 standard; DNA; 20 BP.  
XX  
AC AAV09174;  
XX  
DT 09-JUN-1998 (first entry)  
XX  
DE Phosphorothioate oligonucleotide sequence 8051 targeting ILIR mRNA.  
XX  
XX Type I interleukin-1 receptor; ILIR; human; ILI protein; hybridisation;  
KM inflammation; ss; 5' Cap region; phosphorothioate linkage.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH modified\_base 1..20  
FT /tag= a  
FT /note= "Phosphorothioate internucleotide linkage"  
XX  
XX MO9744656-A1.  
XX  
PD 27-NOV-1997.  
XX  
PF 12-MAY-1997; 97MO-US007147.  
XX  
PR 21-MAY-1996; 96US-00651692.  
XX  
PA (ISIS-) ISIS PHARM INC.  
XX  
PI Miraglia L, Bennett CF, Dean N, Geiger T;  
DR WPI; 1998-018646/02.  
XX  
PT 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor  
PT type I - used to modulate expression and detect overexpression of the  
PT receptor.  
XX  
PS Example 5; Page 19; 63pp; English.  
XX  
XX This is a novel oligomer comprising 20 covalently linked nucleotides  
CC which bind to the 5' Cap region of the interleukin-1 receptor (ILIR)  
CC mRNA. Expression of ILIR in cells and tissues can be modulated by  
CC compositions comprising oligomers which are able to specifically  
CC hybridise with target areas of its encoding sequence. The composition can  
CC be used for treatment of disease in humans caused by excessive receptor  
CC expression, e.g. inflammation. When labelled they can be used  
CC diagnostically to determine overexpression of ILIR, also to determine  
CC localisation and distribution of this expression for research, diagnostic  
CC or therapeutic purposes  
XX  
SQ Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;  
Query Match 2.3%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 373 GGAGTGGCGGCT 386  
|||||

Db 7 GGGCTGCGGCGCT 20

RESULT 8  
AAV09175  
ID AAV09175 standard; DNA; 20 BP.  
XX  
XX AAV09175;  
AC  
XX  
XX 09-JUN-1998 (first entry)  
DT  
XX  
DE Phosphorothiate oligonucleotide sequence 8054 targeting IL1R mRNA.  
XX  
XX Type I interleukin-1 receptor; IL1R; human; IL1 protein; hybridisation;  
KM inflammation; ss; 5' Cap region; phosphorothiate linkage.  
XX  
XX Synthetic.  
OS Homo sapiens.  
XX

Key Location/Qualifiers  
FT modified\_base 1..20  
FT /tag= a  
FT /note= "Phosphorothicate internucleotide linkage"  
XX  
XX WO9744656-A1.  
XX  
XX 27-NOV-1997.  
XX  
XX 12-MAY-1997; 97WO-US007147.  
XX  
XX 21-MAY-1996; 96US-00651692.  
XX  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Miraglia L, Bennett CF, Dean N, Geiger T;  
XX  
XX WPI; 1998-018646/02.  
XX  
XX 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor  
PT Type I - used to modulate expression and detect overexpression of the  
FT receptor.  
XX  
XX Example 5; Page 19; 63pp; English.  
XX  
XX This is a novel oligomer comprising 20 covalently linked nucleotides  
CC which bind to the 5' Cap region of the interleukin-1 receptor (IL1R)  
CC mRNA. Expression of IL1R in cells and tissues can be modulated by  
CC compositions comprising oligomers which are able to specifically  
CC hybridise with target areas of its encoding sequence. The composition can  
CC be used for treatment of disease in humans caused by excessive receptor  
CC expression, e.g. inflammation. When labelled they can be used  
CC diagnostically to determine overexpression of IL1R, also to determine  
CC localisation and distribution of this expression for research, diagnostic  
CC or therapeutic purposes  
XX  
XX Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 2.3%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGGCTGCGGCGCT 386  
Db 2 GGGCTGCGGCGCT 15

RESULT 9  
ABZ30588/c  
ID ABZ30588 standard; DNA; 20 BP.  
XX  
XX ABZ30588;  
AC  
XX  
XX 30-JAN-2003 (first entry)  
DT

XX  
XX Candida albicans GRACE strain PCR primer SEQ ID NO 4739.  
DE  
XX  
XX Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;  
KM signal transduction; DNA replication; cell division; growth;  
KM proliferation; Candida albicans; fungicide; antifungal; PCR; primer; ss.  
XX  
XX Candida albicans.  
OS  
XX WO200253728-A2.  
XX  
XX 11-JUL-2002.  
XX  
XX 26-DEC-2001; 2001WO-US049486.  
XX  
XX 29-DEC-2000; 2000US-0259128P.  
XX  
XX 20-FEB-2001; 2001US-00792024.  
XX  
XX 22-AUG-2001; 2001US-0314050P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KU;  
XX  
XX WPI; 2002-566694/60.  
XX  
XX Constructing strains for identifying gene products as effective targets  
PT for therapeutic intervention, by inactivating in the strain one allele of  
FT a gene and placing other allele of the gene under conditional expression.  
XX  
XX Claim 36; SEQ ID NO 4739; 167pp + Sequence listing; English.  
XX  
XX The invention relates to constructing (M1) a strain of diploid fungal  
CC cells in which both alleles of a gene are modified, comprising modifying  
CC one allele by insertion or replacement by a cassette having an  
CC expressible selectable marker and modifying other allele by  
CC recombination, of a promoter replacement fragment with a heterologous  
CC promoter, so that expression of the second allele is regulated by the  
CC promoter. (M1) is useful for constructing a strain of diploid fungal  
CC cells in which both alleles of a gene are modified. The diploid fungal  
CC cells having both alleles modified are useful for identifying a gene that  
CC is essential to the survival or growth of a fungus, a gene that  
CC contributes to the virulence and/or pathogenicity of a fungus, a gene  
CC that contributes to the resistance of a diploid fungus to an antifungal  
CC agent, an antifungal agent that inhibits the growth of a diploid fungus  
CC and for identifying a therapeutic agent for treatment of a mammalian  
CC disease. (M1) is useful for identifying a compound which modulates the  
CC activity of a gene product, preferably enzymatic activity, carbon  
CC compound catabolism, biosynthetic, transporter, transcriptional,  
CC translational, signal transduction, DNA replication and cell division  
CC activity. The method is useful for identifying a compound having the  
CC ability to inhibit growth or proliferation of C. albicans cells and for  
CC treating infection by C. albicans. The present sequence is that of a PCR  
CC primer used in the method of the invention. Note: The sequence data for  
CC this patent is not represented in the printed specification but is based  
CC on sequence information supplied to Derwent by the European Patent Office  
XX  
XX Sequence 20 BP; 3 A; 5 C; 6 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 2.3%; Score 14; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 352 GACCGCAGGCTGA 365  
Db 14 GACCGCAGGCTGA 1

RESULT 10  
ACA90226  
ID ACA90226 standard; DNA; 20 BP.  
XX  
XX ACA90226;  
AC  
XX  
XX

DT 10-JUL-2003 (first entry)  
 XX  
 DE Novel human protein identification related primer #13.  
 XX  
 KW Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer; NOV; PCR;  
 KW primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003031571-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 02-OCT-2002; 2002WO-US031357.  
 XX  
 PR 05-OCT-2001; 2001US-0327454P.  
 PR 09-OCT-2001; 2001US-0327917P.  
 PR 09-OCT-2001; 2001US-0328029P.  
 PR 09-OCT-2001; 2001US-0328056P.  
 PR 12-OCT-2001; 2001US-0328499P.  
 PR 15-OCT-2001; 2001US-0329414P.  
 PR 17-OCT-2001; 2001US-0330142P.  
 PR 22-OCT-2001; 2001US-0341058P.  
 PR 24-OCT-2001; 2001US-0343629P.  
 PR 29-OCT-2001; 2001US-0349575P.  
 PR 01-NOV-2001; 2001US-0346357P.  
 PR 25-JUN-2002; 2002US-0391342P.  
 PR 01-OCT-2002; 2002US-00262445.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A;  
 PI Edinger SR, Gerlach VL, Giot L, Gorman L, Guo X, Kekuda R;  
 PI Mezes PS, Millet I, Ooi CE, Paturajan M, Rieger DK, Spytek KA;  
 PI Taupier RJ, Zeehuse BD, Zhong H, Zhong M;  
 XX  
 DR WPI; 2003-381704/36.  
 XX  
 PT New DAPK3 polypeptide, useful for preparing a composition for treating or  
 PT preventing e.g., cancer.  
 XX  
 PS Example 20C; Page 212; 253pp; English.  
 XX  
 CC The invention describes an isolated polypeptide comprising any of 33 90-  
 CC 1773 amino acid sequences (I) given in the specification or its mature  
 CC form, a sequence that is at least 95 % identical to (I), or a sequence  
 CC comprising one or more conservative substitutions in the amino acid  
 CC sequence of (I). The polypeptide is useful for preparing a composition  
 CC for treating or preventing e.g. cancer. This sequence represents a primer  
 CC used to isolate DNA encoding a novel human NOV protein  
 XX  
 SO Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.3%; Score 14; DB 7; Length 20;  
 DB Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PS 551 ATGAGGTGATGAC 564  
 DB 1 ATGAGGTGATGAC 14  
 XX  
 RESULT 11  
 ID ADG26512 standard; DNA; 20 BP.  
 XX  
 AC ADG26512;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE NOV protein-related forward PCR primer SEQ ID 337.  
 XX  
 KW NOV; cytostatic; metabolic disorder; immune; neurodegenerative;

KW circulatory; haemopoietic; wasting; cancer; gene therapy; vaccine;  
 KW transgenic; human; ss; PCR; primer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003004687-A2.  
 XX  
 PD 16-JAN-2003.  
 XX  
 PF 03-JUL-2002; 2002WO-US021361.  
 XX  
 PR 05-JUL-2001; 2001US-0303046P.  
 PR 09-JUL-2001; 2001US-0303828P.  
 PR 09-JUL-2001; 2001US-0304016P.  
 PR 11-JUL-2001; 2001US-0304502P.  
 PR 13-JUL-2001; 2001US-0305262P.  
 PR 16-JUL-2001; 2001US-0305673P.  
 PR 17-JUL-2001; 2001US-0306085P.  
 PR 24-JUL-2001; 2001US-0307536P.  
 PR 27-JUL-2001; 2001US-0308282P.  
 PR 30-JUL-2001; 2001US-0308877P.  
 PR 01-AUG-2001; 2001US-0309255P.  
 PR 17-AUG-2001; 2001US-0313388P.  
 PR 12-SEP-2001; 2001US-0318711P.  
 PR 19-SEP-2001; 2001US-0323380P.  
 PR 21-SEP-2001; 2001US-0323969P.  
 PR 04-JAN-2002; 2002US-0345022P.  
 PR 04-JAN-2002; 2002US-0345038P.  
 PR 28-FEB-2002; 2002US-0351172P.  
 PR 01-MAR-2002; 2002US-0360814P.  
 PR 01-MAR-2002; 2002US-0360830P.  
 PR 01-MAR-2002; 2002US-0361133P.  
 PR 05-MAR-2002; 2002US-0361147P.  
 PR 05-MAR-2002; 2002US-0361677P.  
 PR 02-APR-2002; 2002US-0363637P.  
 PR 12-APR-2002; 2002US-037236P.  
 PR 16-APR-2002; 2002US-0372990P.  
 PR 19-APR-2002; 2002US-0373881P.  
 PR 19-APR-2002; 2002US-0373921P.  
 PR 02-JUL-2002; 2002US-00188186.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Anderson DM, Berghs C, Boldog FL, Burgess CE, Casman SJ;  
 PI Catterton E, Edinger S, Eisen AJ, Ellerman K, Gerlach V, Gorman L;  
 PI Guo X, Jeffers M, Kekuda R, Li L, Malyanar UM, Miller CE;  
 PI Padigaru M, Paturajan M, Pena CE, Raetelli L, Shenoy S;  
 PI Shimkets RA, Spaderma SK, Spytek KA, Stone DV, Taupier RJ;  
 PI Vernet CM, Voss EZ, Zhong M;  
 XX  
 DR WPI; 2003-221607/21.  
 XX  
 PT New isolated NOVX polypeptide, useful for determining the presence of, or  
 PT predisposition to a disease associated with altered levels of expression  
 PT of the polypeptide, and for treating or preventing cancer.  
 XX  
 PS Example C; SEQ ID NO 337; 478pp; English.  
 XX  
 CC The invention relates to a novel isolated NOV polypeptide. The  
 CC polypeptide of the invention demonstrates cytostatic activity and may be  
 CC used for determining the presence of, or predisposition to a disease  
 CC associated with altered levels of expression of the polypeptide,  
 CC including metabolic disorders, immune disorders, neurodegenerative  
 CC disorders, circulatory diseases, haemopoietic disorders, wasting diseases  
 CC and cancer. The polypeptide may also be utilised during gene therapy  
 CC procedures, vaccine development and transgenic animal production. The  
 CC current sequence is that of the PCR primer of the invention which was  
 CC used to analyse human NOV DNA.  
 XX  
 SO Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.3%; Score 14; DB 9; Length 20;  
 DB Best Local Similarity 100.0%; Pred. No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CTGCTACGACTGTG 271  
 |||||  
 Db 6 CTGCTACGACTGTG 19

RESULT 12  
 ABT05327  
 ID ABT05327 standard; DNA; 15 BP.

AC ABT05327;  
 DT 24-OCT-2002 (first entry)  
 XX Human N-acetylglucosaminidase (NAGA) alpha gene ASO primer 19.  
 XX  
 KM Human; PCR; primer; ss; gene therapy; N-acetylglucosaminidase alpha;  
 KM chromosome 22q13.2-q13.31; lysosomal glycosidase; screening; SNP;  
 KM NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;  
 KM genotyping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200194637-A1.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 07-JUN-2001; 2001WO-US018456.  
 XX  
 PR 07-JUN-2001; 2000US-0210110P.  
 XX  
 XX (GENA-) GENAISSANCE PHARM INC.  
 PA  
 PI Duda A, Kazemi A, Koshy B, Parks KE;  
 XX  
 DR WPI; 2002-566449/60.  
 XX  
 PT New genetic variants of isolated N-acetylglucosaminidase (NAGA), Alpha  
 PT gene, useful for therapeutic purposes, for studying the expression and  
 PT function of the polymorphic site, and for expressing NAGA protein.  
 XX  
 PS Claim 16; Page 13; 91pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequence of the human N  
 CC -acetylglucosaminidase (NAGA) alpha protein. The invention specifically  
 CC comprises novel polymorphic sites identified within the NAGA gene. The  
 CC NAGA gene is located on chromosome 22q13.2-q13.31 and encodes a  
 CC lysosomal glycosidase that cleaves alpha-N-acetylglucosaminyl  
 CC monomers in glycosylated substrates. The NAGA DNA and protein sequences of the  
 CC invention are useful for studying the expression and function of NAGA and  
 CC for screening candidate drugs to treat diseases related to NAGA activity.  
 CC The NAGA gene polymorphisms identified in the present invention are  
 CC useful for haplotyping and genotyping the NAGA gene of an individual. The  
 CC present DNA sequence represents an N-acetylglucosaminidase gene allele-  
 CC specific oligonucleotide primer  
 XX  
 SQ Sequence 15 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 1 Other;

Query Match 2.2%; Score 13; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 ATTGCTCTCTC 186  
 |||||  
 Db 1 ATTGCTCTCTC 13

RESULT 13  
 ABK24744  
 ID ABK24744 standard; DNA; 17 BP.  
 XX  
 AC ABK24744;

XX 09-APR-2002 (first entry)  
 DT  
 XX  
 DE Glycosate resistance conferring genome altering oligonucleotide #104.  
 XX  
 KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KM o-methyl modification; LNA modification; phosphorothioate linkage;  
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KM abiotic stress tolerance; improved nutritional value; hygromycin-B;  
 KM amino acid over production; herbicide resistance; glyphosate resistance;  
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;  
 KM modified oil production; modified starch production; waxy starch;  
 KM altered floral morphology; male-sterile plant; albino mutant;  
 KM modified fatty acid content; reduced palmitate production; albino plant;  
 KM increased stearate production; reduced linoleic acid production;  
 KM photosynthetic process.  
 XX  
 OS Hordeum vulgare.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200192512-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 01-JUN-2001; 2001WO-US017672.  
 XX  
 PR 01-JUN-2001; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818675.  
 XX  
 XX (UYDE ) UNITV DELAWARE.  
 PA  
 PI Kmlec EB, Gamper HB, Rice MC, Kim J;  
 XX  
 DR WPI; 2002-106307/14.  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 PS Claim 7; Page 51; 220pp; English.  
 XX  
 CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyrin herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).  
 CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGAGACCT 82  
 |||||  
 DB 2 CGCGGTGAGACCT 14

RESULT 14  
 ABRK24743/c  
 ID ABRK24743 standard; DNA; 17 BP.  
 AC ABRK24743;  
 DT 09-APR-2002 (first entry)  
 XX  
 XX  
 DE Glycosate resistance conferring genome altering oligonucleotide #103.

KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;  
 KM o-methyl modification; LNA modification; phosphorothioate linkage;  
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;  
 KM abiotic stress tolerance; improved nutritional value; hygromycin; primer;  
 KM amino acid over production; herbicide resistance; glyphosate resistance;  
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;  
 KM porphyric herbicide resistance; triazine resistance; disease resistance;  
 KM modified oil production; modified starch production; waxy starch;  
 KM altered floral morphology; male-sterile plant; albino mutant;  
 KM modified fatty acid content; reduced palmitate production; albino plant;  
 KM increased stearate production; reduced linoleic acid production;  
 KM photosynthetic process.  
 OS Hordeum vulgare.  
 OS Synthetic.  
 PN WO200192512-A2.  
 PD 06-DEC-2001.  
 XX  
 XX 01-JUN-2001; 2001WO-US017672.  
 PF  
 XX 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 PR 27-MAR-2001; 2001US-00818875.  
 XX  
 XX (UYDE ) UNIV DELMARRE.  
 PA Kmiec EB, Gampier HB, Rice MC, Kim J;  
 PI WPI; 2002-106307/14.  
 DR  
 XX  
 PT New oligonucleotides with modified nuclease-resistant termini, useful for  
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved  
 PT nutritional value, herbicide or disease resistance, or modified oil  
 PT production.  
 XX  
 PS Claim 7; Page 51; 220pp; English.

CC The invention relates to an oligonucleotide for targeted alteration of a  
 CC genetic sequence, which comprises a single-stranded oligonucleotide  
 CC having a DNA domain. The DNA domain has at least one mismatch with  
 CC respect to the genetic sequence to be altered and further comprises  
 CC chemical modifications of the oligonucleotide. The chemical modifications  
 CC consist of o-methyl modification, an LNA modification, two or more  
 CC phosphorothioate linkages on a terminus, or a combination of any two or  
 CC more of these modifications. The oligonucleotides are useful for  
 CC directing repair or alteration of plant genetic information. The  
 CC oligonucleotides are particularly useful for creating plants with desired  
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved  
 CC nutritional value (e.g. altering amino acid content of plants or  
 CC conferring amino acid over production), herbicide resistance (e.g.  
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide  
 CC resistance, porphyric herbicide resistance or triazine resistance),  
 CC disease resistance, modified oil production, modified starch production  
 CC (e.g. increased starch or production of waxy starch), altered floral  
 CC morphology (e.g. male-sterile plants) or modified fatty acid content  
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).

CC The oligonucleotides are also useful for producing albino mutants for the  
 CC analysis of photosynthetic processes. This sequence represents a genome  
 CC altering oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Fred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CGCGGTGAGACCT 82  
 |||||  
 DB 16 CGCGGTGAGACCT 4

RESULT 15  
 ABRV79549/c  
 ID ABRV79549 standard; DNA; 17 BP.  
 AC ABRV79549;  
 XX  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPPL scanning oligonucleotide SEQ ID 795.  
 XX  
 XX Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;  
 KM human testis expressed Patched like protein; testis; adrenal; liver;  
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX EP1229046-A2.  
 PN  
 XX 07-AUG-2002.  
 PD  
 XX 28-JAN-2002; 2002EP-00001167.  
 PF  
 XX 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 PI Zhan J;  
 XX  
 XX WPI; 2002-676582/73.  
 DR  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPPL.  
 XX  
 PS Example 2; Page 168; 718pp; English.

CC The present invention relates to human testis expressed Patched like  
 CC protein (HTPPL, see ABRV78759 to ABRV78762 and ABR88519 to ABR96520). HTPPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPPL-8 (S for short) compared to HTPPL-L (L for long). HTPPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is  
 CC important in regulating male germ cell development, and the HTPPL gene was  
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 9 G; 2 T; 0 U; 0 Other;  
 CC  
 Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 385 CTGCACCGCGCCG 397  
 DB 17 CTGCACCGCGCCG 5  
 XX  
 RESULT 16  
 ID ABV79553/c  
 AC ABV79553 standard; DNA; 17 BP.  
 XX  
 AC ABV79553;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPPL scanning oligonucleotide SEQ ID 799.  
 XX  
 KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;  
 KM human testis expressed Patched like protein; testis; adrenal; liver;  
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPPL.  
 XX  
 PS Example 2; Page 168; 718pp; English.  
 XX  
 PS The present invention relates to human testis expressed Patched like  
 PS protein (HTPPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is  
 CC important in regulating male germ cell development, and the HTPPL gene was  
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human  
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention  
 XX  
 SQ Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;  
 CC  
 Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 385 CTGCACCGCGCCG 397  
 DB 13 CTGCACCGCGCCG 1  
 XX  
 RESULT 17  
 ID ABV79551/c  
 AC ABV79551 standard; DNA; 17 BP.  
 XX  
 AC ABV79551;  
 XX  
 DT 03-JAN-2003 (first entry)  
 XX  
 DE Human HTPPL scanning oligonucleotide SEQ ID 797.  
 XX  
 KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;  
 KM human testis expressed Patched like protein; testis; adrenal; liver;  
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;  
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 EN EP1229046-A2.  
 XX  
 PD 07-AUG-2002.  
 XX  
 PF 28-JAN-2002; 2002EP-00001167.  
 XX  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 23-MAY-2001; 2001US-00864761.  
 PR 09-OCT-2001; 2001US-0327898P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Zhan J;  
 XX  
 DR WPI; 2002-676582/73.  
 XX  
 PT Novel isolated human testis expressed Patched like protein (HTPPL), useful  
 PT for identifying agonist and antagonist and specific binding partners, and  
 PT for treating subjects having defects in HTPPL.  
 XX  
 PS Example 2; Page 168; 718pp; English.  
 XX  
 PS The present invention relates to human testis expressed Patched like  
 PS protein (HTPPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPPL  
 CC has two isoforms, with a few single base pair differences between the  
 CC two. One of the single base pair changes introduces a premature stop  
 CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL  
 CC shares an overall structure organisation with the Patched protein. The  
 CC shared structural features strongly imply that HTPPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is  
 CC important in regulating male germ cell development, and the HTPPL gene was  
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

QY Query Match 2.2%; Score 13; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 15 CTGCACCGCGCCG 3

RESULT 18

ID ABV79552/c

AC ABV79552;

DT 03-JAN-2003 (first entry)

DE Human HTPPL scanning oligonucleotide SEQ ID 798.

XX Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KM male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX prostatic; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX EPI229046-A2.

XX 07-AUG-2002.

PF 28-JAN-2002; 2002EP-00001167.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

PA (AEOM-) AEOMICA INC.

PI Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPPL.

XX Example 2; Page 168; 718pp; English.

XX The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPPL

CC important in regulating male germ cell development, and the HTPPL gene was

CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPPL, and in

CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human

CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,

CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are

CC clinically useful diagnostic markers and potential therapeutic agents for

CC male infertility and cancer. The present oligonucleotide was used in an

XX example from the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

QY Query Match 2.2%; Score 13; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 14 CTGCACCGCGCCG 2

RESULT 19

ID ABV79550/c

AC ABV79550;

DT 03-JAN-2003 (first entry)

DE Human HTPPL scanning oligonucleotide SEQ ID 796.

XX Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

KW human testis expressed Patched like protein; testis; adrenal; liver;

KM male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX prostatic; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

XX EPI229046-A2.

XX 07-AUG-2002.

PF 28-JAN-2002; 2002EP-00001167.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

PA (AEOM-) AEOMICA INC.

PI Zhan J;

XX WPI; 2002-676582/73.

XX Novel isolated human testis expressed Patched like protein (HTPL), useful

PT for identifying agonist and antagonist and specific binding partners, and

PT for treating subjects having defects in HTPPL.

XX Example 2; Page 168; 718pp; English.

XX The present invention relates to human testis expressed Patched like

CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPPL

CC has two isoforms, with a few single base pair differences between the

CC two. One of the single base pair changes introduces a premature stop

CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL

CC shares an overall structure organisation with the Patched protein. The

CC to that of Patched, and is a potential tumour suppressor. HTPPL is

CC shared structural features strongly imply that HTPPL plays a role similar  
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is  
 CC important in regulating male germ cell development, and the HTPPL gene was  
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are  
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in  
 CC therapy and manufacture of a medicament for treatment or prevention of  
 CC such disorder associated with decreased expression or activity of human  
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and  
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,  
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are  
 CC clinically useful diagnostic markers and potential therapeutic agents for  
 CC male infertility and cancer. The present oligonucleotide was used in an  
 CC example from the invention

SO Sequence 17 BP; 2 A; 4 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCGG 397  
 |||||  
 DB 16 CTGCACCGCGCGG 4

RESULT 20

ABL31517  
 ID ABL31517 standard; DNA; 17 BP.

AC ABL31517;

DT 21-MAR-2002 (first entry)

XX Human HLA genotyping oligonucleotide SEQ ID NO 1006.

XX Human; human leukocyte antigen; HLA; genotype; polymorphism;

XX immunogenetic; transplantation; genetic disease; ss.

OS Homo sapiens.

PN WO200192572-A1.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-0P004662.

PS 01-JUN-2000; 2000JP-00164798.

PA (NISON) NISSHINBO IND INC.

PA (SYST-) SYSTEM RES INC.

PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;

PI WPI; 2002-122074/16.

PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of

PT individuals e.g. by determining immunogenetic differences when

PT transplanting between them.

PS Claim 10; Page 284; 345pp; Japanese.

CC The invention relates to a typing kit for judging human leukocyte antigen  
 CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base  
 CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of  
 CC genes e.g. belonging to HLA class I antigens on human genome and  
 CC containing gene polymorphisms as allantoins have been immobilised as  
 CC primers for amplification of cleaved nucleic acids relating to gene  
 CC polymorphisms. The method is useful for judging HLA genotypes of  
 CC individuals by determining immunogenetic differences before transplanting  
 CC between them, providing genetic information to decide compatibility of  
 CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,  
 CC pancreas, Langerhans islet in pancreas and cornea, susceptibility  
 CC diagnosis of genetic diseases and identifying individuals

XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCCACGCTGG 172  
 |||||  
 DB 3 GGCTGCCACGCTGG 15

RESULT 21

ACC53277  
 ID ACC53277 standard; DNA; 17 BP.

AC ACC53277;

DT 27-JUN-2003 (first entry)

XX Human tumour suppressor sequence #2044.

XX ss; tumour suppressor; antitumour; cytosstatic; tumour suppression;

XX tumour regression; apoptosis; virus resistance; diagnosis;

XX cellular degeneration.

OS Homo sapiens.

PN FR826373-A1.

PD 27-DEC-2002.

PF 20-JUN-2001; 2001FR-00008139.

PS 20-JUN-2001; 2001FR-00008139.

PA (MOLE-) MOLECULAR ENGINES LAB SA.

PA Tufjander M, Telerman A, Amson R;

PI WPI; 2003-250498/25.

PT New nucleic acid sequences associated with tumor suppression, regression,

PT apoptosis or virus resistance are useful to diagnose and treat viral

PT disease, development of tumor cells and cell degeneration.

PS Claim 1; Page 512; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated

XX with tumour suppression or regression, apoptosis or virus resistance. The

XX invention relates to these sequences or sequences having at least 80%

XX identity to them, and polypeptides encoded by the sequences or

XX polypeptides having 80% identity to the polypeptide sequences. The

XX invention is used to diagnose or treat viral disease or disease

XX characterized by development of tumour cells or cellular degeneration

XX Sequence 17 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATCCTTTTCACTG 132  
 |||||  
 DB 2 ATCCTTTTCACTG 14

RESULT 22  
 ADA99326/C  
 ID ADA99326 standard; DNA; 17 BP.  
 AC ADA99326;  
 XX



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XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 316; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match      2.2%; Score 13; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 246 CTCCTGGAGCCCC 258
XX 14 CTCCTGGAGCCCC 2
XX
XX RESULT 25
XX ADA9324/c
XX ID ADA9324 standard; DNA; 17 BP.
XX AC ADA9324;
XX AD 20-NOV-2003 (first entry)
XX DT
XX DE Human MD23 scanning oligonucleotide SEQ ID 313.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX

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```

XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 313; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match      2.2%; Score 13; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 246 CTCCTGGAGCCCC 258
XX 17 CTCCTGGAGCCCC 5
XX
XX RESULT 26
XX ADA9328/c
XX ID ADA9328 standard; DNA; 17 BP.
XX AC ADA9328;
XX AD 20-NOV-2003 (first entry)
XX DT
XX DE Human MD23 scanning oligonucleotide SEQ ID 317.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 317; 103pp; English.
XX

```

CC The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MD23,  
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
CC alterations can also be used as probes to detect and characterize gross  
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;  
SQ

Query Match 2.2%; Score 13; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 246 CTCCTGAGCCCC 258  
DB 13 CTCCTGAGCCCC 1

RESULT 27  
ABZ61946/c  
ID ABZ61946 standard; RNA, 17 BP.  
XX  
XX ABZ61946;  
XX  
XX 21-MAR-2003 (first entry)  
XX  
XX Human H-Ras DNAzyme target #737.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297114-A2.  
XX  
XX MCSwigen J;  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US016840.  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
XX 06-JUN-2001; 2001US-0296249P.  
XX 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX MCSwigen J;  
XX  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 125; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytoskeletal, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences  
CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

XX Sequence 17 BP; 1 A; 6 C; 5 G; 0 T; 5 U; 0 Other;  
SQ

Query Match 2.2%; Score 13; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 GCAAGGCTGAGCC 368  
DB 15 GCAAGGCTGAGCC 3

RESULT 28  
ABZ61384  
ID ABZ61384 standard; RNA, 17 BP.  
XX  
XX ABZ61384;  
XX  
XX 21-MAR-2003 (first entry)  
XX  
XX Human H-Ras DNAzyme target #175.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytoskeletal; anti-HIV;  
XX anti-rheumatic; cancer; AIDS; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200297114-A2.  
XX  
XX MCSwigen J;  
XX  
XX 05-DEC-2002.  
XX  
XX 29-MAY-2002; 2002WO-US016840.  
XX  
XX 29-MAY-2001; 2001US-0294140P.  
XX 06-JUN-2001; 2001US-0296249P.  
XX 10-SEP-2001; 2001US-0318471P.  
XX  
XX (RIBO-) RIBOZYME PHARM INC.  
XX  
XX MCSwigen J;  
XX  
XX WPI; 2003-140484/13.  
XX  
XX Novel short interfering RNA and enzymatic nucleic acid useful for  
XX treating cancer, modulates the expression of a nucleic acid encoding  
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX Claim 58; Page 114; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic  
CC acid molecule or an enzymatic nucleic acid molecule, that modulates  
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,  
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic  
CC acid molecule of the invention has cytoskeletal, anti-HIV, and anti-  
CC rheumatic activity. The nucleic acid molecules are useful for reducing  
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are  
CC also useful for treating breast, ovarian, colorectal, lung, prostate,  
CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,  
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human  
CC ribozymes of the invention

XX Sequence 17 BP; 0 A; 5 C; 11 G; 0 T; 1 U; 0 Other;  
SQ

Query Match 2.2%; Score 13; DB 7; Length 17;  
Best Local Similarity 92.3%; Pred. No. 3.8e+04;  
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGCGG 384  
 |||||  
 DB 3 GGGGCTGCGCGG 15

RESULT 29  
 AA244774/C  
 ID AA244774 standard; DNA; 18 BP.

AC AA244774;

DT 19-APR-2000 (first entry)

DE Human FADD primer ISIS #23874.

KM FADD; human; antisense; inhibitor; Fas-associated death domain; primer;  
 KW probe; ss.

OS Homo sapiens.

PN US6015712-A.

PD 18-JAN-2000.

PF 19-JUL-1999; 99US-00357072.

PR 19-JUL-1999; 99US-00357072.

PA (ISIS-) ISIS PHARM INC.

PI Mona BP, Cowser LM, Baker BF, Zhang H;

DR WPI; 2000-126316/11.

PT Antisense oligonucleotides, useful for inhibiting human Fas-associated  
 death domain (FADD) expression are targeted to the 3' untranslated region  
 of the FADD gene.

PS Example 16; Col 53-54; 37pp; English.

CC This invention describes novel antisense oligonucleotides (OGNs) (I) 8-20  
 CC nucleotides in length that specifically hybridize with and inhibit  
 CC nucleic acids encoding human Fas-associated death domain (FADD), targeted  
 CC to the 3' untranslated region (3'UTR). (I) can be used to treat animals,  
 CC especially humans, suspected of having or being prone to a disease or  
 CC condition associated with FADD expression. AA244746-244831 represent  
 CC primers and probes used in the method of the invention

SQ Sequence 18 BP; 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGGACTTTGGTT 142  
 |||||  
 DB 14 CTGGACTTTGGTT 2

RESULT 30  
 AA241855/C  
 ID AA241855 standard; cDNA; 19 BP.

AC AA241855;

DT 21-FEB-1997 (first entry)

DE Probe/primer for Plasmodium falciparum erythrocyte membrane protein.

KM Plasmodium falciparum; erythrocyte membrane protein; malaria; detection;  
 KW identification; treatment; prevention; parasite; ss.

OS Synthetic.

XX W09633736-A1.

XX 31-OCT-1996.

XX 26-APR-1996; 96WO-US005798.

XX 27-APR-1995; 95US-00430908.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Baruch DI, Pastoske BL, Howard RJ;

XX WPI; 1996-497376/49.

PT New Plasmodium falciparum erythrocyte membrane proteins - used to develop  
 PT products for the diagnosis, treatment or prevention of malaria parasite  
 PT infections.

PS Disclosure; Page 24; 149pp; English.

CC A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte  
 CC membrane protein 1 (PfEMP1) or active fragments or analogues of that  
 CC protein can be used in the treatment or prevention of symptoms of that  
 CC malaria parasite infection. The polypeptides can inhibit, block or  
 CC reverse the sequestration of erythrocytes in patients suffering from  
 CC malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes  
 CC and primers to identify a Plasmodium falciparum parasite, the primers  
 CC used to generate characteristic amplification patterns from different P.  
 CC falciparum strains. Antibodies specifically immunoreactive with the  
 CC PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria  
 CC infection. Nucleic acid fragments of at least 15 contiguous nucleotides  
 CC of the PfEMP1 gene are also claimed. They may be generated by  
 CC amplification with the probes/primers described in AA241854-241867

SQ Sequence 19 BP; 8 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCCTCCCA 520  
 |||||  
 DB 15 GTTCGTCCTCCCA 3

RESULT 31  
 AA283045/C  
 ID AA283045 standard; DNA; 19 BP.

AC AA283045;

DT 04-DEC-2000 (first entry)

DE cdk6 ribozyme binding site #105.

KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

PN W0200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

PA (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.  
XX PS Disclosure; Page 55; 109pp; English.  
XX CC The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AA82415 to AA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment  
XX SQ Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;  
XX  
XX Query Match 2.2%; Score 13; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 481 GCCTGGAGAGGC 493  
DB 17 GCCTGGAGAGGC 5  
XX  
XX RESULT 32  
AA83046/c  
ID AA83046 standard; DNA; 19 BP.  
XX AC AA83046;  
XX DT 04-DEC-2000 (first entry)  
XX DE cdk6 ribozyme binding site #106.  
XX DE cdk6 ribozyme binding site #106.  
XX KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.  
XX OS Mammalia.  
XX PN WO200032765-A2.  
XX PD 08-JUN-2000.  
XX PF 06-DEC-1999; 99WO-US028772.  
XX PR 04-DEC-1998; 98US-0110954P.  
XX PA (IMMU-) IMMUSOL INC.  
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;  
XX WPI; 2000-412314/35.  
XX DR  
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves  
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,  
PT PCNA and Cyclin B1.  
XX PS Disclosure; Page 55; 109pp; English.  
XX CC The present invention relates to a hairpin or hammerhead ribozyme,  
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase  
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.  
CC Representative examples of ribozyme recognition sites are given in  
CC AA82415 to AA86787. The ribozyme of the invention is useful for  
CC inhibiting restenosis by introduction of the ribozyme into cells. The  
CC ribozyme is resistant to endonuclease activity and hence is efficient in  
CC restenosis treatment  
XX SQ Sequence 19 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;  
XX  
XX Query Match 2.2%; Score 13; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 481 GCCTGGAGAGGC 493  
DB 16 GCCTGGAGAGGC 4  
XX  
XX RESULT 33  
AA165672/c  
ID AA165672 standard; DNA; 19 BP.  
XX AC AA165672;  
XX DT 03-JAN-2002 (first entry)  
XX DE Primer for studying biallelic polymorphic markers in the IBD1 region.  
XX KM Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;  
KM intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;  
KM inflammatory disease; immune disease; cryptogenic inflammation;  
KM hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.  
XX OS Homo sapiens.  
XX PN FR2806739-A1.  
XX PD 28-SEP-2001.  
XX PF 27-MAR-2000; 2000FR-00003832.  
XX PR 27-MAR-2000; 2000FR-00003832.  
XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.  
XX PI Hugot JP, Thomas G, Zouali M, Lesage S, Chamaillard M;  
XX WPI; 2001-608364/70.  
XX DR  
XX PT New human nucleic acids associated with intestinal inflammatory disease,  
PT useful for diagnosis, prognosis and control of these diseases, also  
PT related proteins.  
XX PS Example 4; Page 88; 97pp; French.  
XX CC Primers AA165647-78 were used to characterise biallelic polymorphic  
CC markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory  
CC bowel disease 1 (IBD1) polypeptide, which is associated with intestinal  
CC inflammatory disease. The specification also describes a polypeptide  
CC which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene  
CC is probably involved in regulation of apoptosis and activation of NF-  
CC kappa B. The IBD1 and IBD1prox polynucleotides are useful as source of  
CC probes and primers, as source of (anti)sense oligonucleotides, for  
CC recombinant production of polypeptides, and in screening for interactive  
CC compounds. The polypeptides are used to raise specific antibodies which  
CC useful for diagnostic detection or purification of IBD1 and IBD1prox, to  
CC screen for specific binding agents, potential therapeutic agents. The  
CC IBD1 and IBD1prox polynucleotides and polypeptides are useful for  
CC treatment and prevention of inflammatory and/or immune diseases or  
CC cancer, where associated with mutations in genes corresponding to IBD1  
CC and IBD1prox, especially with mutations in genes corresponding to the intestines  
CC (hemorrhagic rectocolitis, Crohn's disease and Blau syndrome)  
XX SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
XX  
XX Query Match 2.2%; Score 13; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 53 TCCGCTGGGCTAA 65  
DB 18 TCCGCTGGGCTAA 6

RESULT 34	AAH58207/	standard; DNA, 19 BP.
ID	AAH58207	
AC	AAH58207	
XX		
XX	10-SEP-2001	(first entry)
DT		
XX		
DE	Cell-cycle dependent kinase cdk6 ribozyme binding site SHQ ID NO:631.	
XX		
KM	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;	
KM	recognition site; target; ribozyme binding site; eye disease; vulnery;	
KM	proliferative disease; skin disease; psoriasis; diabetic retinopathy;	
KM	cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;	
KM	matrix metalloproteinase; growth factor; redutcase; scarring; cytostatic;	
KM	antiproliferative; dermatological; antiseborrheic; antidiabetic; vituide;	
KM	antiscarring; ophthalmological; keratolytic; gene therapy; viral wart;	
KM	atopic dermatitis; actinic keratosis; squamous cell carcinoma;	
KM	basal cell carcinoma; seborehic wart; vitreoretinopathy; scar;	
KM	sickle cell retinopathy; ss.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	WO200130362-A2.	
XX		
PD	03-MAY-2001.	
XX		
PF	26-OCT-2000; 2000MC-US029500.	
XX		
PR	26-OCT-1999; 99US-0161532P.	
XX		
PA	(IMMU-) IMMUSOL INC.	
XX		
PL	Robbins JM, Tritz R;	
PL		
DR	WPI; 2001-300427/31.	
XX		
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes	
PT	that cleave RNA encoding cytokines involved in inflammation, matrix	
PT	metalloproteinases, growth factors and cell-cycle dependent kinases.	
XX		
PS	Example 1; Page 117; 408pp; English.	
XX		
CC	The present invention describes a method for treating a proliferative	
CC	skin or eye disease and scarring. The method involves administering a	
CC	ribozyme (I) which cleaves RNA encoding a cytokine involved in	
CC	inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle	
CC	dependent kinase, growth factor or a reductase, or administering a	
CC	nucleic acid molecule (II) comprising a promoter operably linked to a	
CC	nucleic acid segment encoding (I). (I) can have antipsoriatic,	
CC	dermatological, cytotratic, antiseborrheic, antidiabetic, antiscikling,	
CC	ophthalmological, vulnery, keratolytic and vituide activities, and	
CC	cleaves RNA encoding cytokine involved in inflammation. (I) can be used	
CC	in gene therapy. (I) and (II) are useful for treating proliferative skin	
CC	diseases such as psoriasis, atopic dermatitis, actinic keratosis,	
CC	squamous or basal cell carcinoma and viral or seborehic wart. They can	
CC	also be used for treating proliferative eye diseases such as diabetic	
CC	retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of	
CC	prematurity, and retinal detachment, and for treating and preventing	
CC	scarring such as keloid, adhesion and hypertrophic or hypertrophic burn	
CC	scar. AAH57577 to AAH62099 represent sequences used in the	
XX	exemplification of the present invention	
XX		
Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;		

```

Query Match      2.2%; Score 13; DB 5; Length 19;
Best Local Similarity 100.0%; Pred.No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY      481 GCCTGGGAAGGCG 493

```

Db 17 GCCTGGGAAGGC 5

RESULT 35  
AAH58208/c  
ID AAH58208 standard; DNA; 19 BP.  
XX  
AC AAH58208;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:632.

Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;  
recognition site; target; ribozyme binding site; eye disease; vulnery;  
proliferative disease; skin disease; psoriasis; diabetic retinopathy;  
cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;  
matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;  
antiproliferative; dermatological; antidiabetic; vitamin D;  
antiangiogenic; ophthalmological; keratolytic; gene therapy; viral wart;  
acopic dermatitis; actinic keratosis; squamous cell carcinoma;  
basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;  
sickle cell retinopathy; ss.

XX Homo sapiens.  
OS Synthetic.  
XX  
XX WC2001.03062-A2.  
XX  
XX 03-MAY-2001.  
XX  
XX 26-OCT-2000; 200OWO-US0295500.  
XX  
XX 26-OCT-1999; 99US-0161532P.  
XX  
XX (IMMUT.) IMMUGOL INC.  
XX  
XX Robbin JM, Tritz R;  
XX  
XX WPI; 2001-300427/31.  
XX

Treating proliferative skin or eye diseases and scarring, using ribozymes  
that cleave RNA encoding cytokines involved in inflammation, matrix  
metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 118; 400BP; English.

The present invention describes a method for treating a proliferative  
skin or eye disease and scarring. The method involves administering a  
ribozyme (I) which cleaves RNA encoding a cytokine involved in  
inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle  
dependent kinase, growth factor or a reductase, or administering a  
nucleic acid molecule (II) comprising a promoter operably linked to a  
nucleic acid segment encoding (I). (I) can have anti-proliferative,  
ophthalmological, cytostatic, antiseborrheic, antidiabetic, anti-skinning,  
dermatological, vulnerary, keratolytic and vitamin activities, and  
cleaves RNA encoding cytokine involved in inflammation. (I) can be used  
in gene therapy. (I) and (II) are useful for treating proliferative skin  
diseases such as psoriasis, acopic dermatitis, actinic keratosis,  
squamous or basal cell carcinoma and viral or seborrheic wart. They can  
also be used for treating proliferative eye diseases such as diabetic  
retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of  
prematurity and retinal detachment, and for treating and preventing  
scarring such as keloid adhesion and hypertrophic or hypertrophic burn  
scar. AAH57577 to AAH6209 represent sequences used in the  
exemplification of the present invention

SQ Sequence 19 Bp, 2 A, 7 C, 6 G, 4 T, 0 U, 0 Other;  
 Query Match 2.2%; Score 13; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Qy 481 GCCTGGAGAGGC 493  
 Db 16 GCCTGGAGAGGC 4

RESULT 36  
 ACF03639/C  
 ID ACF03639 standard; DNA; 19 BP.

AC ACF03639;  
 XX  
 DT 15-SEP-2003 (first entry)  
 XX  
 DE Human NOV13 forward PCR primer SEQ ID NO:209.

Human; NOVX; cytostatic; cardiac; anti-inflammatory; immunosuppressive;  
 KM anti-allergic; haemostatic; anti-HIV; antidiabetic; antidiarrhetic; hepatocytic;  
 KM anorectic; antiaesthetic; nephrotoxic; antitachytic; hepatocytic;  
 KM neuroprotective; nootropic; antibacterial; virucide; antiparasitic;  
 KM relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;  
 KM vulnery; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;  
 KM cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;  
 KM autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;  
 KM acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;  
 KM Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;  
 KM muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.

OS Homo sapiens.  
 OS Synthetic.  
 PN WO200294870-A2.  
 PD 28-NOV-2002.  
 XX  
 PF 02-NOV-2001; 2001MO-US051580.  
 XX  
 PR 02-NOV-2000; 2000US-0245291P.  
 PR 02-NOV-2000; 2000US-0245317P.  
 PR 07-NOV-2000; 2000US-0246562P.  
 PR 08-NOV-2000; 2000US-0246871P.  
 PR 26-JAN-2001; 2001US-0264389P.  
 PR 26-JAN-2001; 2001US-0264423P.  
 PR 29-JAN-2001; 2001US-0264799P.  
 XX  
 PA (CURA-) CURAGEN CORP.

Grosse WM, MacDougall JR, Smithson G, Miller I, Stone DJ;  
 PI Gunther E, Ellerman K, Alsebrook JP, Lepley DM, Burgess CE;  
 PI Spytek KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L;  
 PI Guo X, Fernandes ER, Vernet CM, Tchervet VT, Casman SJ, Shenoy S;  
 PI Mishra V, Furtak K, Baumgartner JC, Colman SD.  
 DR WPI; 2003-140359/13.  
 XX  
 PT New NOVX polypeptide useful for preventing or treating NOVX-associated  
 PT disorder, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and  
 PT in chromosome mapping, tissue typing or pharmacogenomics.  
 XX  
 PS Example 2, Page 316, 346pp; English.

ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABB57412  
 CC to ABB57435. (I) have cytostatic, cardiac, anti-inflammatory, nootropic,  
 CC immunosuppressive, antitachytic, haemostatic, anti-HIV, antidiabetic,  
 CC antidiarrhetic, anorectic, antiaesthetic, nephrotoxic, virucide,  
 CC antiparasitic, hepatocytic, neuroprotective, antibacterial, relaxant,  
 CC antiparkinsonian, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,  
 CC vulnery, angiogenic and antiangiogenic activities, and can be used in  
 CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can  
 CC be used to determine the presence or absence of (I) in a sample. The NOVX  
 CC polypeptides, polynucleotides encoding them, and antibodies against them,  
 CC are useful in manufacturing a medicament for treating or preventing a  
 CC syndrome associated with a NOVX-associated disorder such as hypertension,  
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,

CC autoimmune disorders, allergies, blood disorders, obesity, acquired  
 CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) A nephropathy,  
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,  
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular  
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic  
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX  
 CC sequence, which are used in an example from the present invention

XX  
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query March 2.2%; Score 13; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 487 GAAGGCTGCATG 499  
 Db 17 GAAGGCTGCATG 5

RESULT 37  
 AAQ71065  
 ID AAQ71065 standard; DNA; 20 BP.  
 XX  
 AC AAQ71065;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 19-APR-1995 (first entry)  
 XX  
 DE Primer #1 to generate STS 96r7 for identification of the merlin gene.

XX  
 KM Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
 KM sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
 KM neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D2S28;  
 KM tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
 KM merlin-associated tumour; D2S21; posterior capsular lens opacity;  
 KM deafness; balance disorder; paralysis; ss.

OS Synthetic.  
 PN EP613945-A2.  
 PD 07-SEP-1994.  
 XX  
 PR 25-FEB-1994; 94BP-00301367.  
 PR 25-FEB-1993; 93US-00022034.  
 PR 04-MAR-1993; 93US-00026063.  
 PR 19-AUG-1993; 93US-00108808.  
 PR 22-DEC-1993; 93US-00171718.  
 XX  
 PA (GENO) GEN HOSPITAL CORP.

Trofatter JA, Maccollin MM, Gusella JF;  
 PI WPI; 1994-272992/34.  
 DR The tumour suppressor gene merlin - for treatment and diagnosis of  
 PT tumours and neurofibromatosis (NF2).  
 XX  
 PS Disclosure; Page 3; 86pp; English.

XX  
 CC The sequences given in AAQ71063-66 are primers which were used in a  
 CC sequence-tagged site assay of the region of chromosome 22 surrounding the  
 CC NF2 deletions. NF2 is a neurofibromatosis which is characterised by bi-  
 CC lateral schwannomas. The NF2 "gene" has been shown by linkage studies to  
 CC be assigned to chromosome 22. The missing or mutated gene in NF2 patients  
 CC has been shown to be the merlin gene. The gene encodes a protein, merlin  
 CC (moesin-erzin-radixin-like protein), which possesses tumour suppressor  
 CC activity, and whose tumour suppressor activity is mediated by  
 CC interactions with the cytoskeleton. The merlin gene is found on  
 CC chromosome 22 between the known markers D2S1 and D2S28. The merlin gene  
 CC may be used in gene therapy for the treatment of a merlin-associated  
 CC tumour or NF2, or for prevention of schwannoma, meningioma, posterior

CC	capsular lens opacities; deafness or hearing loss; balance disorders or paralysis. (Updated on 25-MAR-2003 to correct FN field.)
XX	
SQ	Sequence 20 BP; 5 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
OY	
DB	118 ACATCCTTTTCAC 130       8 ACATCCTTTTCAC 20
Query Match	2.2%; Score 13; DB 2; Length 20; Best Local Similarity 100.0%; Pred.No.3.8e+04;
Matches	13; Conservative 0; Mismatches 0; Indels 0; Gaps 0
RESULT 38	
ID	AAV68469 standard; DNA; 20 BP.
XX	
AC	AAV68469;
XX	
DT	22-MAR-1999 (first entry)
XX	
DE	Oligo contained activator-antisense complex spa+-anti-(M3)hTR.
XX	
KW	Human; telomerase; hTR; activator-antisense complex; malignant; enzyme;
KW	Cleave; brain; tumour malignant glioma; breast tumour; renal cell cancer;
KW	melanoma; prostate cancer; leukemia; polychemia vera; myeloma; sarcoma;
KW	Hodgkin's lymphoma; Waldenstrom's macroglobulinemia; heavy chain disease;
KW	carcinoma; chemotherapeutic; antisense; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	1
FT	/tag= a
FT	/note= "Sp5'A(2'p5'A)3-Bu2"
FT	19..20
FT	/tag= b
FT	/note= "3'-3' internucleotide linkage"
FT	20
FT	/tag= c
FT	/note= "nucleotide in reverse orientation 3'-5'"
XX	
PN	WO9847911-A1.
XX	
PD	29-OCT-1998.
PF	13-APR-1998; 98WO-US007397.
XX	
PR	21-APR-1997; 97US-0044507P.
XX	
PR	03-FEB-1998; 98US-00018125.
PA	(CLEAV-) CLEVELAND CLINIC FOUND.
XX	
PI	(USSH ) US NAT INST OF HEALTH.
XX	
PI	Silverman RH, Kondo S, Cowell JK, Li G, Torrence PF;
DR	WPI, 1998-603972/51.
PT	New RNase L activator-telomerase antisense complex - useful to inhibit
PT	telomerase activity in telomerase-expressing malignancies.
XX	
PS	Example; Page 45; 81pp; English.
CC	This represents an antisense oligonucleotide to the RNA component of
CC	human telomerase (hTR) comprised in the. The invention relates to an
CC	activator-antisense complex that comprises: (a) an antisense oligo,
CC	complementary to a 12-25 nucleotide portion of the RNA component of hTR,
CC	with a hydroxyl moiety at the first end; and (b) a linker attached to the
CC	first end; and (c) an activator of RNase L attached to the linker. The
CC	activator-antisense complex may be used for inhibiting the growth of a
CC	telomerase-expressing malignant cell or tumour. The complex is used to

CC specifically cleave the ribonucleotide portion of a telomerase enzyme.  
 CC The complex inhibits growth of telomerase expressing malignant cells from  
 CC brain tumour malignant glioma, breast tumour, renal cell cancer,  
 CC melanoma, and prostate cancer. Many other malignancies and related  
 CC disorders, may be treated including various acute and chronic leukemias,  
 CC polycythemia vera, Hodgkin's and non-Hodgkin's lymphomas, multiple  
 CC myeloma, Waldenström's macroglobulinemia, heavy chain disease, and solid  
 CC tumours, including numerous sarcomas and carcinomas. The complex is  
 CC preferably administered in combination with a chemotherapeutic agent,  
 CC particularly either cisplatin, doxorubicin, mitomycin, daunorubicin,  
 CC bleomycin, actinomycin D, or neocarzinostatin. The present sequence is an  
 CC example of a modified antisense oligo comprised in an activator-antisense  
 CC complex spA4-anti-(M3)hTR

XX  
 SQ Sequence 20 BP, 4 A, 6 C, 7 G, 3 T, 0 U, 0 Other;

XX  
 Query Match 2.2%; Score 13; DB 2; Length 20;  
 XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407  
 XX |||||  
 DB 3 CCGGGGTGCAAT 15

RESULT 39  
 ID AAZ37511/c  
 XX AAZ37511 standard; DNA; 20 BP.  
 XX AC  
 XX AAZ37511;  
 XX  
 DT 07-JAN-2000 (first entry)  
 XX  
 DE Human mdm2 phosphorothioate oligodeoxynucleotide #41.  
 XX  
 KW Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;  
 KW antisense; modulation; oligonucleotide; expression; inhibition;  
 KW hyperproliferation; blood cancer; brain cancer; breast cancer;  
 KW lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;  
 KW resection; ss.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 OS  
 PN WO9943065-A1.  
 PN  
 PD 30-SEP-1999.  
 XX  
 PF 26-MAR-1999; 99WO-US006702.  
 XX  
 PR 26-MAR-1998; 98US-00048810.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett IM;  
 XX  
 DR WPI; 1999-610754/52.  
 XX  
 PT New antisense compounds used to treat eg. hyperproliferative conditions.  
 XX  
 PS Example 9; Page 47; 157pp; English.  
 XX  
 CC AAZ37473-4237738 represent human mdm2 phosphorothioate oligonucleotides.  
 CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the  
 CC exemplification of the present invention. The present invention describes  
 CC novel nucleotide antisense compounds, targeted to the 5' untranslated,  
 CC translation termination codon, or 3' untranslated region of a nucleic  
 CC acid encoding human mdm2, that modulates expression of human mdm2. The  
 CC oligonucleotides mediate their effect by antisense inhibition of  
 CC hyperproliferative gene expression. The antisense compound is used to  
 CC treat an animal having a disease or condition associated with mdm2,  
 CC particularly a hyperproliferative condition, more particularly cancer,  
 CC especially of the blood, brain, breast, lung or soft tissue, or

CC peoriasis, fibrosis, atherosclerosis or restenosis

XX Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;

SQL Query Match 2.2%; Score 13; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376

DB 19 GAGCCCGAGGGGC 7

RESULT 40

AA87306 AAX87306 standard; DNA; 20 BP.

XX AAX87306;

XX 27-SEP-1999 (first entry)

XX PRO509 reverse PCR primer 50148.tm.rl.

XX PRO509; cancer; tumour; diagnosis; therapy; human; PCR; primer; ss.

XX Synthetic.

XX Homo sapiens.

XX MO935170-A2.

XX 15-JUL-1999.

XX 05-JAN-1999; 99MO-US000106.

XX 05-JAN-1998; 98US-0070440P.

XX 29-APR-1998; 98US-0083500P.

XX 22-MAY-1998; 98US-0086414P.

XX 10-JUN-1998; 98US-0088742P.

XX 10-NOV-1998; 98US-0107833P.

XX 20-NOV-1998; 98US-0109304P.

XX (GETH ) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;

XX Wood WI;

XX WPI; 1999-430385/36.

XX Antibody against proteins expressed in neoplastic cells, useful for tumor

XX diagnosis and treatment.

XX Example 2; Page 55; 162pp; English.

XX This is the nucleotide sequence of reverse primer 50148.tm.rl that can be

XX used in the PCR amplification of DNA50148 (see AAX87265) nucleic acids

XX coding for PRO509 (see AAY06488). This gene is amplified in various

XX tumour lines. The invention identifies 14 genes (see AAX87254-67) that

XX are amplified in the genome of certain human lung, colon and/or breast

XX cancers and/or cell lines. This gene amplification is expected to be

XX associated with overexpression of the gene product and to contribute to

XX tumorigenesis. The encoded proteins (see AAY06477-90) may be useful

XX targets for the diagnosis and/or treatment of certain cancers, and may

XX act as predictors of the prognosis of tumour treatment

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

XX Query Match 2.2%; Score 13; DB 2; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 2 TGGACAGCCTCTT 14

XX DB 6 TGGACAGCCTCTT 18

RESULT 41

AAA8137/c AAA8137 standard; DNA; 20 BP.

XX AAA8137;

XX 30-AUG-2000 (first entry)

XX Polynucleotide used for ddl gene detection.

XX D alanine:D alanine ligase; ddl, detect; Streptococcus; Enterococcus; ss.

XX Streptococcus sp.

XX US6054269-A.

XX 25-APR-2000.

XX 25-JUN-1997; 97US-00882501.

XX 25-JUN-1997; 97US-00882501.

XX (INSP ) INST PASTEUR.

XX Garnier F, Gerbaud G, Dutka-Malen S, Charles M, Evers S;

XX Casadewall B, Gailmand M, Courvalin P;

XX WPI; 2000-338486/29.

XX New polynucleotides derived from unknown sequences internal to the ddl

XX genes coding for D-Alanine:D-Alanine ligase of various bacterial strains

XX belonging to Enterococci or Streptococci genus, useful as probes.

XX Claim 2; Col 57; 42pp; English.

XX Sequences AAA8133-A38148 represent polynucleotides that hybridise with a

XX nucleic acid sequence encoding a D-alanine:D-alanine ligase of a given

XX species belonging to the Streptococci or Enterococci species. The

XX polynucleotides are used to detect bacteria belonging to the Streptococci

XX and Enterococci genus in a sample. The polynucleotides are also used as

XX probes or primers that are specific for particular species or groups of

XX species belonging to Streptococci or Enterococci genus. The

XX oligonucleotide probes are also useful as capture probes immobilized on a

XX substrate to capture a target nucleic acid and can be used in a detection

XX device comprising a matrix library of probes immobilized on a substrate

XX Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

XX Query Match 2.2%; Score 13; DB 3; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 335 GCCTCTACTTCTG 347

XX DB 15 GCCTCTACTTCTG 3

XX RESULT 42

XX AAC60546/c AAC60546 standard; DNA; 20 BP.

XX ID AAC60546

XX AAC60546;

XX 31-JAN-2001 (first entry)

XX Human fra-1 mRNA antisense oligonucleotide ISIS 109037.

XX Human fra-1; antisense oligonucleotide; phosphorothioate; cytosatic;

XX antiinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;

XX ss.



```

PS Example 9; Col 27; 77bp; English.
XX
CC The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
XX
SQ Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.2%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7
XX
RESULT 45
ID AAS29280 standard; DNA; 20 BP.
XX
AC AAS29280;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31716.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
XX
PN 23-AUG-2001.
XX
PD 02-JAN-2001; 2001US-00752983.
XX
PF 26-MAR-1998; 98US-00048810.
XX
PR 26-MAR-1999; 99US-00280805.
XX
PA (MIRA/) MIRAGLIA L J.
PA (NERO/) NERO P.
PA (GRAH/) GRAHAM M J.
PA (MONI/) MONIA B P.
PA (COMS/) COMSERT L M.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Comsert LM;
XX
DR WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
PT nucleobases targeted a region (e.g. translation termination codon region)
PT of a nucleic acid encoding human mdm2.
XX
XX Example 9; Page 15; 81bp; English.
XX
CC The present invention relates to antisense compounds, 8-30 nucleobases in
CC length targeted to the 5' untranslated region, translation termination
CC codon region, 3' untranslated region, coding region or translation start

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CC site of a nucleic acid encoding human mdm2, where the antisense compound
CC modulates the expression of human mdm2. The antisense oligonucleotides of
CC the invention are useful for encoding human mdm2 and for inhibiting the
CC expression of human mdm2. They may be used for treating an animal having
CC a disease or condition associated with amplification of mdm2 gene or
CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC and chronic myelogenous leukemia. The antisense compound may be
CC administered with a chemotherapeutic agent to overcome drug resistance.
CC The antisense compound reduces hyperproliferation of human cells. The
CC method, which involves the use of the antisense compound, is also useful
CC for detecting the role of mdm2 expression in various cell functions and
CC physiological processes and useful in both clinical research and
CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC oligonucleotides of the present invention
XX
SQ Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.2%; Score 13; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7
XX
RESULT 46
ID AAL42131 standard; DNA; 20 BP.
XX
AC AAL42131;
XX
XX 27-MAY-2002 (first entry)
XX
DE Human KLF6 gene exon 2 PCR primer 2AF3.
XX
XX Human; PCR; primer; ss; Kruppel-like factor 6; KLF6; 2AF3;
XX tumour suppressor gene; cancer risk; prostate cancer; neuroblastoma;
XX glioblastoma; melanoma; breast cancer; ovarian cancer;
XX squamous cell carcinoma; hepatocellular cancer; lung cancer;
XX colon cancer; benign hyperplasia; gene therapy.
XX
XX Homo sapiens.
XX
OS Hemo sapiens.
XX
PN WO200212894-A1.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US025046.
XX
PR 09-AUG-2000; 2000US-022411P.
XX
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX
PI Friedman S, Li D, Naria G, Martignetti J, Heath K;
XX
DR WPI; 2002-241784/29.
XX
XX Detecting inactivation or alteration of a Kruppel-like factor 6 (KLF6)
PT gene, useful for diagnosing or determining the relative risk of a cancer
PT (e.g. neuroblastoma or breast cancer) by detecting modifications of the
PT KLF6 genomic DNA.
XX
XX Example 7; Page 63; 103bp; English.
XX
CC The invention comprises a method for detecting a modification in genomic
CC DNA, causing inactivation or alteration of a Kruppel-like factor 6 (KLF6)
CC tumour suppressor gene. The method of the invention is useful for
CC diagnosing, prognosing or determining the relative risk of a cancer (i.e.
CC prostate cancer, neuroblastoma, glioblastoma, melanoma, breast cancer,
CC ovarian cancer, head and neck squamous cell carcinoma, hepatocellular

```

CC cancer, lung cancer, or colon cancer. The method is also useful for  
 CC preventing or treating human hyperplasia (e.g. benign hyperplasia), or  
 CC cancers. The KLF6 gene sequence is useful for expressing the KLF6 protein  
 CC in somatic cell types for human gene therapy. The present sequence  
 CC represents a PCR primer specific for the human KLF6 gene sequence  
 XX  
 SQ Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 TTTTGCCCTGTA 551  
 |||||  
 DB 3 TTTTGCCCTGTA 15

## RESULT 47

AA040381  
 ID AA040381 standard; DNA; 20 BP.

XX  
 AC AA040381;

XX 19-SEP-2002 (first entry)

DE Mouse caspase 6 antisense inhibition related oligo SEQ ID No 100.

XX Muscular; cytoskeletal; nocotropic; neuroprotective; ophthalmological;  
 KM antileptemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;  
 KM ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;  
 KM haematopoietic disorder; cancer; neurological; Alzheimer's disease;  
 KM apoptotic; mouse; murine; de.

XX Mus musculus.

PN WO200229066-A1.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030871.

XX 04-OCT-2000; 2000US-00679299.

XX (ISIS-) ISIS PHARM INC.

PI Brown-Driver VL, Zhang H, Watt AT;

DR WPI; 2002-471315/50.

PT An antisense oligonucleotide of 8 to 50 nucleotides in length that  
 PT inhibits caspase 6, is useful for treating Rieger's syndrome.

PS Claim 3; Page 91; 141pp; English.

XX The invention relates to an antisense oligonucleotide compound of 8 to 50  
 CC nucleotides in length that is targeted to a nucleic acid molecule  
 CC encoding caspase 6, where the oligonucleotide specifically hybridises  
 CC with and inhibits the expression of caspase 6. The oligonucleotide of the  
 CC invention specifically hybridises to and inhibits expression of caspase 6  
 CC in cells or tissues. The oligonucleotides can be administered  
 CC therapeutically or prophylactically to treat an animal having a disease  
 CC or condition associated with caspase 6, such as Rieger's syndrome or  
 CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic  
 CC disorder, a bone metabolism or cholesterol disorder, various types of  
 CC cancer, neurological conditions such as Alzheimer's disease and other de-  
 CC regulated apoptotic pathological conditions. This polynucleotide sequence  
 CC represents a mouse caspase 6 oligonucleotide relating to the invention.  
 CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOB wings and  
 CC a deoxy gap

SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match

2.2%; Score 13; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 447 TACTTTGTAGAA 459  
 |||||  
 DB 4 TACTTTGTAGAA 16

## RESULT 48

ABK70785/c  
 ID ABK70785 standard; DNA; 20 BP.

XX  
 AC ABK70785;

XX 15-JUL-2002 (first entry)

DE Human TSPI domain containing gene sequencing primer KY01-518.

XX TSPI; thrombospondin domain; DNA sequencing; primer; ss; FG06969;  
 KM FG01896; angiogenesis; vasculogenesis.

XX Homo sapiens.

PN JP2002085059-A.

PD 26-MAR-2002.

XX 08-SEP-2000; 2000JP-00273778.

XX 08-SEP-2000; 2000JP-00273778.

XX (KAZU-) ZH KAZUSA DNA KENKYUSHO.

XX (YOSH ) YOSHITOMI PHARM IND KK.

DR WPI; 2002-378268/41.

PT TSPI domain-containing polypeptide useful for drug compositions.

PS Example 2; Page 15; 51pp; Japanese.

XX The invention relates to a TSPI (thrombospondin 1) domain-containing  
 CC polypeptide comprising the proteins appearing as AA080188 and AA080189,  
 CC encoded by cDNAs designated FG06969 and FG01896. Also included are  
 CC proteins that are 50% homologous to the proteins and a polypeptide having  
 CC at least one deletion, replacement, addition or insertion of amino acid  
 CC in the protein and having at least 8 repetitions of the TSPI domain. The  
 CC polypeptide can be used in drug compositions particularly for disorders  
 CC associated with angiogenesis and vasculogenesis. The present sequence is  
 CC a sequencing primer for the cDNAs of the invention

SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 ACCTAGACCTGG 218  
 |||||

DB 15 ACCTAGACCTGG 3

## RESULT 49

AA046719/c  
 ID AA046719 standard; DNA; 20 BP.

XX  
 AC AA046719;

DT 20-AUG-2002 (first entry)

DE Human serine-threonine protein kinase coding sequence PCR primer #1.

XX Human; serine-threonine protein kinase; cancer; diabetes; obesity;  
 KM central nervous system disorder; inflammation; gene therapy; COPD;

KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;  
 KW antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;  
 KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;  
 KW PCR; enzyme; primer; ss.  
 XX Homo sapiens.  
 XX WO200233056-A2.  
 XX  
 XX 25-APR-2002.  
 XX  
 XX 15-OCT-2001; 2001WO-EP011892.  
 XX  
 XX 16-OCT-2000; 2000US-02400972.  
 XX 30-JUL-2001; 2001US-0308096D.  
 XX  
 XX (FARB ) BAYER AG.  
 XX  
 XX Koehler RH;  
 XX  
 XX WPI; 2002-435534/46.  
 XX  
 XX New human serine-threonine protein kinase and encoding polynucleotides,  
 PT useful for diagnosing, treating and preventing central nervous system  
 PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).  
 XX  
 XX Example 11; Page 95; 135pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of a  
 CC human serine-threonine protein kinase. The sequences can be used in the  
 CC diagnosis, treatment and prevention of cancers (e.g. leukemia, lymphoma  
 CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or  
 CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,  
 CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and  
 CC chronic obstructive pulmonary disease (COPD). The present sequence is a  
 CC PCR primer for the coding sequence of the invention  
 XX  
 XX Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.2%; Score 13; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 194 TCTCGACTGGGA 206  
 Db 19 TCTCGACTGGGA 7  
 RESULT 50  
 ACC49244  
 ID ACC49244 standard; DNA; 20 BP.  
 XX  
 XX ACC49244;  
 AC  
 XX 20-JUN-2003 (first entry)  
 XX  
 XX Human ribonuclease L antisense oligonucleotide SEQ ID NO:61.  
 DE  
 XX Human; ribonuclease L; antisense modulation; cytostatic; antimicrobial;  
 KW antiinflammatory; antitumor; ribonuclease L expression inhibitor;  
 KW antisense gene therapy; infection; aberrant apoptosis; cancer; tumour;  
 KW inflammation; phosphorothioate; 2'-O-methoxyethyl; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 OS Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH modified\_base 1..20  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "phosphorothioate linkages"  
 FT modified\_base 1..5  
 FT /tag= b

PT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls (2'-MOEs) "  
 FT modified\_base 15..20  
 FT /tag= c  
 FT /mod\_base= OTHER  
 FT /note= "2'-O-methoxyethyls (2'-MOEs) "  
 XX  
 XX WO2003023011-A2.  
 XX  
 XX 20-MAR-2003.  
 XX  
 XX 09-SEP-2002; 2002WO-US0287229.  
 XX  
 XX 12-SEP-2001; 2001US-00954679.  
 XX  
 XX (ISIS-) ISIS PHARM INC.  
 XX  
 XX Ward DT, Watt AT;  
 XX  
 XX WPI; 2003-313248/30.  
 XX  
 XX Novel antisense compound which is targeted to nucleic acid encoding  
 PT ribonuclease L, and inhibits expression of ribonuclease L protein, useful  
 PT for treating diseases or conditions resulting from infections and  
 PT aberrant apoptosis.  
 XX  
 XX Claim 3; Page 78; 106pp; English.  
 XX  
 XX The present invention describes a compound (I) of 8-50 nucleobases in  
 CC length targeted to a nucleic acid molecule (II) encoding ribonuclease L  
 CC (III), and which specifically hybridises with (II) and inhibits  
 CC expression of (III), where (I) specifically hybridises with at least an 8  
 CC -nucleobase portion of an active site on (II). (I) has cytostatic,  
 CC antitumoral, antiinflammatory and antitumour activities, and can be  
 CC used as a ribonuclease L expression inhibitor and in antisense gene  
 CC therapy. (I) is useful for inhibiting the expression of ribonuclease L in  
 CC cells or tissues, and for treating an animal having a disease condition  
 CC associated with ribonuclease L, e.g. infection, aberrant apoptosis or  
 CC cancer. (I) is also useful for modulating the process of RNA-mediated  
 CC interference (RNAi) in a cell or animal. (I) is also useful  
 CC prophylactically, e.g. to prevent or delay infection, inflammation or  
 CC tumour formation. (I) is useful as a tool in differential and/or  
 CC combinatorial analyses to elucidate expression patterns of a portion or  
 CC the entire complement of genes expressed within cells and tissues. (I) is  
 CC also useful for research, therapeutics and diagnostics. (I) is also  
 CC useful for distinguishing functions of various members of a biological  
 CC pathway, and in antisense gene therapy. The present sequence represents a  
 CC human ribonuclease L chimeric phosphorothioate antisense oligonucleotide,  
 CC which is used in an example from the present invention  
 XX  
 XX Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.2%; Score 13; DB 7; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 313 AGCTGAGGATCT 325  
 Db 1 AGCTGAGGATCT 13  
 RESULT 51  
 AAD53632/c  
 ID AAD53632 standard; DNA; 20 BP.  
 XX  
 XX AAD53632;  
 AC  
 XX 28-MAY-2003 (first entry)  
 XX  
 XX Human PTPN2 antisense oligonucleotide, ISIS #135690.  
 DE  
 XX Antisense; human; protein tyrosine phosphatase non-receptor type 2;  
 KW PTPN2; autoimmune disorder; hyperproliferative condition; cancer;

[illegible]

KW		library screening; Southern hybridisation; northern hybridisation;
KV		dot blot hybridisation; gene sequence; mutation detection;
KM		target sequence; probe; PCR; primer; ss.
OS		unidentified.
PX		
NN		US2003082596-A1.
PN		
XX		
PF		08-AUG-2002; 2002US-00215112.
PR		08-AUG-2001; 2001US-0311040P.
PA	(MITT)/ MITTMANN M.	
XX		
PI	Mittmann M;	
DR	WIPO / 2003-576608/54.	
XX		
PT	New probe array useful e.g. for monitoring gene expression levels, for analyzing genetic variations, or for hybridizing tag-labeled compounds, comprises multiple nucleic acid probes.	
PS	Claim 1; SEQ ID NO 9359; 3pp; English.	
XX		
CC	The present invention relates to nucleic acid sequences that are complementary to particular genes, and can be used as probes for a variety of analyses such as gene expression analysis. Each probe comprises 9 or more consecutive nucleotides from at least one of 14936 nucleotide sequences defined in the patent, or their perfect sense match, sense mismatch, antisense match or antisense mismatch oligonucleotides. The probes may be used in an array comprising at least 10 distinct nucleic acid probes. The array is useful in monitoring gene expression levels by hybridization to a DNA library, in analysing genetic variations, and in hybridising tag-labelled compounds. The probes are useful for identifying family members of a gene. The probes are also useful in situ hybridizations, in screening cDNA or genomic libraries (or derived sublibraries) for additional clones containing segments of DNA that have been previously isolated and sequenced, in Southern, northern, or dot-blots hybridisation of genomic DNA to identify or detect the presence of any gene or detect specific mutations in any gene, and in mapping the 5' termini of mRNA molecules by primer extensions. The nucleic acid sequences of the invention are also useful as PCR primers. The invention provides a large collection of nucleic acid sequences complementary to particular genes with a wide range of analytical uses. ACHS0865-ACHS5260 represent the target sequences of the invention. Note: the sequence data for this patent was obtained in electronic format directly from the USPTO web site at <a href="#">seqdata.uspto.gov/patididentity.html</a>	
SQ	Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;	
OY	Query Match                2 %; Score 13; DB 8; Length 20; Best Local Similarity     100.0%; Pred. No. 3.8e+04; Matches      13; Conservative      0; Mismatches      0; Indels          0; Gaps            0;	
Dd	77 AGAGCTACTGTG 89         15 AGAGCTACTGTG 3	
RESULT 53		
ID	ACH60616	
XX	ACH60616 standard; DNA; 20 BP.	
AC	ACH60616;	
DT	17-OCT-2003 (first entry)	
XX		
DE	DNA target sequence #9752 useful in array for genetic analyses.	
KW	Gene expression analysis; array; hybridisation; genetic variation;	
KM	tag-labelled compound; gene family; in situ hybridisation;	

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Miltmann M;  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 9752; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/ps/psidbentry.html](http://seqdata.uspto.gov/ps/psidbentry.html)  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 77 AGACCTACTGTG 89  
 6 AGACCTACTGTG 18  
 XX  
 AC ACH60951;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #10087 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Miltmann M;  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 10087; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/ps/psidbentry.html](http://seqdata.uspto.gov/ps/psidbentry.html)  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 77 AGACCTACTGTG 89  
 6 AGACCTACTGTG 18  
 XX  
 AC ACH60952;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #10088 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KM target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Miltmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 10088; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdidentry.html  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 3.8e-04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 77 AGACCTACTCTGTG 89  
 |||||  
 6 AGACCTACTCTGTG 18  
 XX  
 DE DNA target sequence #9863 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KM target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 XX  
 PI Miltmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 9863; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdidentry.html  
 XX  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. NO. 3.8e-04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 77 AGACCTACTCTGTG 89  
 |||||  
 6 AGACCTACTCTGTG 18  
 XX  
 DE DNA target sequence #9583 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX Unidentified.  
 XX OS  
 XX PN US2003082596-A1.  
 XX PD  
 XX PD 01-MAY-2003.  
 XX PF 08-AUG-2002; 2002US-00215112.  
 XX PF 08-AUG-2001; 2001US-0311040P.  
 XX PR (MITT/) MITTMANN M.  
 XX PA Miltmann M;  
 XX PI  
 XX PI WPI; 2003-576608/54.  
 XX DR  
 XX DR New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 9583; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/psipdsidentry.html](http://seqdata.uspto.gov/psipdsidentry.html)  
 XX  
 SO Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 77 AGACCTACTGTG 89  
 Db 15 AGACCTACTGTG 3

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX Unidentified.  
 XX OS  
 XX PN US2003082596-A1.  
 XX PD  
 XX PD 01-MAY-2003.  
 XX PF 08-AUG-2002; 2002US-00215112.  
 XX PF 08-AUG-2001; 2001US-0311040P.  
 XX PR (MITT/) MITTMANN M.  
 XX PA Miltmann M;  
 XX PI  
 XX PI WPI; 2003-576608/54.  
 XX DR  
 XX DR New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 9584; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/psipdsidentry.html](http://seqdata.uspto.gov/psipdsidentry.html)  
 XX  
 SO Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 77 AGACCTACTGTG 89  
 Db 15 AGACCTACTGTG 3

RESULT 58  
 ACH60448/C  
 ID ACH60448 standard; DNA; 20 BP.  
 XX  
 AC ACH60448;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #9584 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

RESULT 59  
 ACH60451/C  
 ID ACH60451 standard; DNA; 20 BP.  
 XX  
 AC ACH60451;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #9587 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 OS Unidentified.  
 XX US2003082596-A1.  
 FN  
 PD 01-MAY-2003.  
 XX  
 XX 08-AUG-2002; 2002US-00215112.  
 PF  
 XX 08-AUG-2001; 2001US-0311040P.  
 PR  
 PA (MITT/) MITTMANN M.  
 XX  
 XX Miltmann M;  
 PI  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 XX Claim 1; SEQ ID NO 9587; 9pp; English.  
 PS  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridizing tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/patidentrty.html](http://seqdata.uspto.gov/patidentrty.html)  
 CC  
 SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 77 AGACCTACTCTGTG 89  
 Db 15 AGACCTACTCTGTG 3  
 XX  
 RESULT 60  
 ACH60955  
 ID ACH60955 standard; DNA; 20 BP.  
 XX  
 AC ACH60955;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #10091 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 OS Unidentified.  
 XX US2003082596-A1.  
 FN  
 PD 01-MAY-2003.  
 XX  
 XX 08-AUG-2002; 2002US-00215112.  
 PF  
 XX 08-AUG-2001; 2001US-0311040P.  
 PR  
 PA (MITT/) MITTMANN M.  
 XX  
 XX Miltmann M;  
 PI  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 XX Claim 1; SEQ ID NO 10091; 9pp; English.  
 PS  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridizing tag-labeled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/patidentrty.html](http://seqdata.uspto.gov/patidentrty.html)  
 CC  
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 XX  
 Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 77 AGACCTACTCTGTG 89  
 Db 6 AGACCTACTCTGTG 18  
 XX  
 RESULT 61  
 ACH60111/c  
 ID ACH60111 standard; DNA; 20 BP.  
 XX  
 AC ACH60111;  
 XX  
 DT 17-OCT-2003 (first entry)  
 XX  
 DE DNA target sequence #9247 useful in array for genetic analyses.  
 XX  
 KW Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN US2003082596-A1.  
 XX  
 PD 01-MAY-2003.  
 XX  
 PF 08-AUG-2002; 2002US-00215112.  
 XX  
 PR 08-AUG-2001; 2001US-0311040P.  
 XX  
 PA (MITT/) MITTMANN M.  
 PI Miltmann M;  
 XX  
 DR WPI; 2003-576608/54.  
 XX  
 PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 XX  
 PS Claim 1; SEQ ID NO 9247; 9pp; English.  
 XX  
 CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACHS0865-ACHS6260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/patseqidentry.html](http://seqdata.uspto.gov/patseqidentry.html)  
 XX  
 SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 2.2%; Score 13; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 77 AGACCTACTGTG 89  
 DB 15 AGACCTACTGTG 3  
 XX  
 RESULT 62  
 ADD21476/C  
 ID ADD21476 standard; DNA; 20 BP.  
 XX  
 AC ADD21476;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human mdm2 antisense oligonucleotide #39.  
 XX  
 KW antisense oligonucleotide; human; mdm2; hyperproliferation;  
 KW hyperproliferative disorder; cancer; psoriasis; fibrosis;  
 KW

KW atherosclerosis; restenosis; apoptosis modulation; p21; ss;  
 KW 2'-methoxyethoxy-residue; phosphorothioate backbone.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003048315-A2.  
 XX  
 PD 12-JUN-2003.  
 XX  
 PF 02-DEC-2002; 2002WO-US038281.  
 XX  
 PR 04-DEC-2001; 2001US-00005344.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 PI Miraglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,  
 PI Manoharan M;  
 XX  
 DR WPI; 2003-577263/54.  
 XX  
 PT Novel antisense compound targeted to 5' untranslated region, coding  
 PT region, or intron:exon junction of nucleic acid molecule encoding mdm2,  
 PT useful for treating e.g. cancer, psoriasis or restenosis by inhibiting  
 PT mdm2 expression.  
 XX  
 PS Example 9; SEQ ID NO 41; 289pp; English.  
 XX  
 CC The invention comprises antisense oligonucleotides which are targeted to  
 CC the human mdm2 gene. The antisense oligonucleotides of the invention are  
 CC useful for reducing hyperproliferation of human cells. The antisense  
 CC oligonucleotides are also useful for treating: hyperproliferative  
 CC disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or  
 CC restenosis. The antisense oligonucleotides are also useful for modulating  
 CC apoptosis, and for increasing expression of p21. The present DNA sequence  
 CC represents a human mdm2 gene antisense oligonucleotide of the invention.  
 CC The present sequence contains 2'-methoxyethoxy-residues and has a  
 CC phosphorothioate backbone.  
 XX  
 SQ Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 2.2%; Score 13; DB 9; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 364 GAGCCCGAGGGGC 376  
 DB 19 GAGCCCGAGGGGC 7  
 XX  
 RESULT 63  
 AB134852/C  
 ID AB134852 standard; DNA; 12 BP.  
 XX  
 AC AB134852;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 334825 for detecting SNP TSC0038427.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX

PA (EPiG-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 334825; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 12 BP; 7 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
 QY  
 Query Match 2.0%; Score 12; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 425 AAGATTATTTT 436  
 12 AAGATTATTTT 1  
 XX  
 RESULT 64  
 AB135151  
 ID AB135151 standard; DNA; 12 BP.  
 AC AB135151;  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 335124 for detecting SNP TSC0038615.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPiG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 335124; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 12 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 0 Other;  
 QY  
 Query Match 2.0%; Score 12; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 424 AAGATTATTTT 435  
 1 AAGATTATTTT 12  
 XX  
 RESULT 65  
 AB160311  
 ID AB160311 standard; DNA; 12 BP.  
 AC AB160311;  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide primer SEQ ID NO 360284 for detecting SNP TSC0052014.  
 XX  
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001WO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPiG-) EPIGENOMICS AG.  
 PI Olek A, Piepenbrock C, Berlin K;  
 PI WPI; 2001-657177/75.  
 XX  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 360284; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 12 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 437  
 |||||  
 DB 1 AGATTATTTT 12

RESULT 66  
 ABH96686/c  
 ID ABH96686 standard; DNA; 12 BP.  
 AC ABH96686;  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide primer SEQ ID NO 296679 for detecting SNP TSC0017210.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX MO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIC-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 296679; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 12 BP; 1 A; 0 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312  
 |||||  
 DB 12 AACCCCAACCTC 1

RESULT 67  
 AB178279  
 ID AB178279 standard; DNA; 12 BP.

XX AB178279;  
 AC  
 XX 22-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide primer SEQ ID NO 378252 for detecting SNP TSC0062690.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX MO200177384-A2.  
 PN  
 XX 18-OCT-2001.  
 PD  
 XX 06-APR-2001; 2001WO-IB000713.  
 PF  
 XX 07-APR-2000; 2000DE-01019173.  
 PR  
 XX (EPIC-) EPIGENOMICS AG.  
 PA  
 XX Olek A, Piepenbrock C, Berlin K;  
 PI  
 XX WPI; 2001-657177/75.  
 DR  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 378252; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 XX Sequence 12 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 436  
 |||||  
 DB 1 AAGATTATTTT 12

RESULT 68  
 ABC01330  
 ID ABC01330 standard; DNA; 13 BP.  
 AC ABC01330;  
 XX 20-FEB-2002 (first entry)  
 DT  
 XX Oligonucleotide SEQ ID NO 1321 for detecting SNP TSC0000450.  
 DE  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS

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PN WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 1321; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 12; DB 4; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 426 AGATTATTTTGA 437
DB 1 AGATTATTTTGA 12
XX
XX RESULT 69
XX ABC54252/C
XX ID ABC54252 standard; DNA; 13 BP.
XX
XX ABC54252;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 54269 for detecting SNP TSC0014903.
XX
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX

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XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 54269; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 8 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
SQ
XX
XX Query Match 2.0%; Score 12; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 428 ATTATTTTACT 439
DB 12 ATTATTTTACT 1
XX
XX RESULT 70
XX ABF95377
XX ID ABF95377 standard; DNA; 13 BP.
XX
XX ABF95377;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 195374 for detecting SNP TSC0048069.
XX
XX SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPiG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 195374; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The

```

CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX  
 CC Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTTACT 439  
 DB 2 ATTATTTTACT 13

## RESULT 71

ABF99192  
 ID ABF99192 standard; DNA; 13 BP.

XX  
 AC ABF99192;

XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 199189 for detecting SNP TSC0049016.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PS Claim 1; SEQ ID NO 199189; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 1 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATATTTTAA 437

DB 1 AGATATTTTAA 12

## RESULT 72

ABH06778/c  
 ID ABH06778 standard; DNA; 13 BP.

XX  
 AC ABH06778;

XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 206755 for detecting SNP TSC0050584.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.

PS Claim 1; SEQ ID NO 206755; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 1 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CAATTCAAAAT 51  
 DB 12 CAATTCAAAAT 1

## RESULT 73

ABH06779  
 ID ABH06779 standard; DNA; 13 BP.

XX  
 AC ABH06779;

XX  
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 206756 for detecting SNP TSC0050584.  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 206756; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 1 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 40 CATTCAAAAT 51  
 DB 2 CATTCAAAAT 13  
 RESULT 74  
 ABF95376/c  
 ID ABF95376 standard; DNA; 13 BP.  
 XX ABF95376;  
 AC 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 195373 for detecting SNP TSC0048069.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 PF

XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX Claim 1; SEQ ID NO 195373; 29pp + Sequence Listing; German.  
 PS  
 XX This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 428 ATTATTTTACT 439  
 DB 12 ATTATTTTACT 1  
 RESULT 75  
 ABF88871/c  
 ID ABF88871 standard; DNA; 13 BP.  
 XX ABF88871;  
 AC 22-FEB-2002 (first entry)  
 XX Oligonucleotide SEQ ID NO 18868 for detecting SNP TSC0046496.  
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 OS Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-IB000713.  
 XX 07-APR-2000; 2000DE-01019173.  
 XX (EPIC-) EPIGENOMICS AG.  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX

PS Claim 1; SEQ ID NO 18868; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 U; 0 Other;  
Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 425 AAGATTATTTT 436  
DB 13 AAGATTATTTT 2  
RESULT 76  
ABF35048/c  
ID ABF35048 standard; DNA; 13 BP.  
AC ABF35048;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 135045 for detecting SNP TSC0033667.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 135045; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 40 CAATCAAAAT 51  
DB 12 CAATCAAAAT 1  
RESULT 77  
ABF51823/c  
ID ABF51823 standard; DNA; 13 BP.  
AC ABF51823;  
XX  
DT 21-FEB-2002 (first entry)  
XX  
DE Oligonucleotide SEQ ID NO 151820 for detecting SNP TSC0038356.  
XX  
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.  
OS Homo sapiens.  
XX  
PN WO200177384-A2.  
XX  
PD 18-OCT-2001.  
XX  
PF 06-APR-2001; 2001WO-IB000713.  
XX  
PR 07-APR-2000; 2000DE-01019173.  
XX  
PA (EPIC-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-657177/75.  
XX  
PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.  
XX  
PS Claim 1; SEQ ID NO 151820; 29pp + Sequence Listing; German.  
XX  
CC This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 5 A; 2 C; 0 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 450 TTTTGTAGAAA 461  
DB 12 TTTTGTAGAAA 1

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RESULT 78
ABC01331/c
ID ABC01331 standard; DNA; 13 BP.
XX
AC ABC01331;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 1322 for detecting SNP TSC0000450.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001MO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 1322; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 426 AGATTATTTTA 437
DB 13 AGATTATTTTA 2

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XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001MO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 113243; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 182 TCCTCCGCTACA 193
DB 13 TCCTCCGCTACA 2

```

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RESULT 79
ABF13246/c
ID ABF13246 standard; DNA; 13 BP.
XX
AC ABF13246;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 113243 for detecting SNP TSC0028347.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

```

```

RESULT 80
ABC22482/c
ID ABC22482 standard; DNA; 13 BP.
XX
AC ABC22482;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 22499 for detecting SNP TSC0004446.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001MO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPiG-) EPIGENOMICS AG.
XX

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PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 2249; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 1 A; 0 C; 8 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Db 301 AACCCCAACCTC 312  
 13 AACCCCAACCTC 2  
 XX  
 RESULT 81  
 ABC54253  
 ID ABC54253 standard; DNA; 13 BP.  
 XX  
 AC ABC54253;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 54270 for detecting SNP TSC0014903.  
 XX  
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WC200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001MO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 54270; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 Db 428 ATTATTTTACT 439  
 2 ATTATTTTACT 13  
 XX  
 RESULT 82  
 ABC75762/C  
 ID ABC75762 standard; DNA; 13 BP.  
 XX  
 AC ABC75762;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 75779 for detecting SNP TSC0019426.  
 XX  
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WC200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 PF 06-APR-2001; 2001MO-IB000713.  
 XX  
 PR 07-APR-2000; 2000DE-01019173.  
 XX  
 PA (EPIC-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2001-657177/75.  
 XX  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 75779; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.0%; Score 12; DB 5; Length 13;



PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 199190; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 0 U; 1 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 426 AGATTATTTT 437  
 DB 13 AGATTATTTT 2  
 RESULT 86  
 ABC22483  
 ID ABC22483 standard; DNA; 13 BP.  
 AC ABC22483;  
 XX  
 DT 20-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 22500 for detecting SNP TSC0004446.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 22500; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 301 AACCCCAACTC 312  
 DB 1 AACCCCAACTC 12  
 RESULT 87  
 ABF51822  
 ID ABF51822 standard; DNA; 13 BP.  
 AC ABF51822;  
 XX  
 DT 21-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 151819 for detecting SNP TSC0038356.  
 XX  
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200177384-A2.  
 XX  
 PD 18-OCT-2001.  
 XX  
 DE 06-APR-2001; 2001WO-IB000713.  
 XX  
 XX 07-APR-2000; 2000DE-01019173.  
 XX  
 XX (EPIG-) EPIGENOMICS AG.  
 XX  
 XX Olek A, Piepenbrock C, Berlin K;  
 XX  
 XX WPI; 2001-657177/75.  
 DR  
 XX  
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 XX Claim 1; SEQ ID NO 151819; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 13 BP; 6 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 450 TTTGTAGAAA 461  
DB 2 TTTGTAGAAA 13

RESULT 88  
ABF88870  
ID ABF88870 standard; DNA; 13 BP.

AC ABF88870;  
XX  
DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 188867 for detecting SNP TSC0046496.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIDENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 188867; 29bp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 425 AAGATTATTTT 436  
XX

DB 1 AAGATTATTTT 12

RESULT 89  
ABH62102/c  
ID ABH62102 standard; DNA; 13 BP.

AC ABH62102;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 262079 for detecting SNP TSC0063588.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIDENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
PT designed to detect single-nucleotide polymorphisms and cytosine  
PT methylation status.

PS Claim 1; SEQ ID NO 262079; 29bp + Sequence listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic  
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
CC and cytosine methylation status in chemically pretreated genomic DNA. The  
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
CC range of diseases including immune system, gastrointestinal, respiratory,  
CC central nervous system, cardiovascular and metabolic disorders. The  
CC oligomers are also used for detecting cell type differentiation. ABC00010  
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
CC represent the oligomers described in the invention. NOTE: The sequence  
CC data for this patent did not form part of the printed specification, but  
CC was obtained in electronic format from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 13 BP; 1 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 301 AACCCCAACCTC 312  
DB 12 AACCCCAACCTC 1

RESULT 90  
ABF35049  
ID ABF35049 standard; DNA; 13 BP.

AC ABF35049;

DT 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 135046 for detecting SNP TSC0033667.

KM SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD  
 PF 06-APR-2001; 2001WO-IB000713.  
 PR 07-APR-2000; 2000DE-01019173.  
 XX (EPig-) EPIGENOMICS AG.  
 PA (EPig-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 135046; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CAATTCAAAAT 51  
 DB 2 CAATTCAAAAT 13  
 RESULT 91  
 ABH62103  
 ID ABH62103 standard; DNA; 13 BP.  
 XX  
 AC ABH62103;  
 XX  
 DT 22-FEB-2002 (first entry)  
 XX  
 DE Oligonucleotide SEQ ID NO 262080 for detecting SNP TSC0063588.  
 XX  
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;  
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;  
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.  
 XX Homo sapiens.  
 OS  
 XX WO200177384-A2.  
 XX 18-OCT-2001.  
 PD  
 PF 06-APR-2001; 2001WO-IB000713.  
 PR 07-APR-2000; 2000DE-01019173.

XX  
 PA (EPig-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX WPI; 2001-657177/75.  
 DR  
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is  
 PT designed to detect single-nucleotide polymorphisms and cytosine  
 PT methylation status.  
 XX  
 PS Claim 1; SEQ ID NO 262080; 29pp + Sequence Listing; German.  
 XX  
 CC This invention describes novel oligonucleotide primers or peptide nucleic  
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)  
 CC and cytosine methylation status in chemically pretreated genomic DNA. The  
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a  
 CC range of diseases including immune system, gastrointestinal, respiratory,  
 CC central nervous system, cardiovascular and metabolic disorders. The  
 CC oligomers are also used for detecting cell type differentiation. ABC00010  
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073  
 CC represent the oligomers described in the invention. NOTE: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 13 BP; 5 A; 7 C; 0 G; 1 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCGACCTC 312  
 DB 2 AACCCGACCTC 13  
 RESULT 92  
 AAD24072/c  
 ID AAD24072 standard; DNA; 13 BP.  
 XX  
 AC AAD24072;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE Arabidopsis thaliana HYS transcription factor binding site.  
 XX  
 KM Gene expression; maize; ubiquitin promoter; Ubi-1; HSE;  
 KM heat shock element; agronomic gene; HYS transcription factor; ds.  
 XX Arabidopsis thaliana.  
 OS  
 XX WO200194394-A2.  
 XX 13-DEC-2001.  
 PD  
 PF 08-JUN-2001; 2001WO-US018689.  
 PR 09-JUN-2000; 2000US-00590558.  
 XX  
 PA (PROD-) PRODIGENE INC.  
 XX  
 PI Jilka JM, Hood BE, Howard JA;  
 XX WPI; 2002-122117/16.  
 DR  
 PT New promoter sequences for causing expression of a structural gene  
 PT especially agronomic gene or open reading frame in a plant cell,  
 PT comprises engineered versions of the maize ubiquitin promoter.  
 XX  
 PS Disclosure; Page 30; 69pp; English.  
 XX  
 CC The invention relates to a promoter sequence capable of directing

CC expression of a nucleotide sequence in a plant cell, comprising maize  
 CC ubiquitin (ubi-1) promoter sequence with a modification so that it does  
 CC not include two overlapping heat shock elements (HSE) or its directs  
 CC expression to increase the endosperm/embryo expression ratio of the  
 CC protein when compared to the ratio from a wild-type ubiquitin promoter.  
 CC The modified ubi-1 promoter comprises a deletion of 3', 5' or both HSEs,  
 CC two non-overlapping/adjacent HSEs, replacement of HSEs with a trimer of a  
 CC seed specific element from the promoter of pea lectin gene Pcl 1, or  
 CC insertion of a transcription factor binding site in the HSE region. An  
 CC expression construct comprising modified ubi-1 promoter is useful for  
 CC causing expression of a structural gene (agronomic genes) or open reading  
 CC frame in a plant cell. The modified ubi-1 promoter increases expression  
 CC levels beyond those observed with native ubiquitin promoter. The present  
 CC sequence is Arabidopsis thaliana H5 transcription factor binding site of  
 CC Ribulose-1,5-bisphosphate carboxylase gene, used in the present invention  
 CC  
 SQ Sequence 13 BP; 2 A; 5 C; 3 G; 3 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 163 TGCCACGTGGA 174  
 DB 13 TGCCACGTGGA 2  
 RESULT 93  
 ID AAT79478/c  
 AC AAT79478 standard; DNA; 14 BP.  
 XX AAT79478;  
 DT 22-OCT-1997 (first entry)  
 DE DNA ligand for adenosine or adenosine 5'-phosphate.  
 XX  
 DE Adenosine; adenosine-5'-phosphate; adenosine triphosphate; ATP; binding;  
 KM ligand; purification; reagent; isolation; determination;  
 KM subcellular localization; catalyst; assay; SELEX;  
 KM Systematic Evolution of Ligands by Exponential enrichment; se.  
 XX  
 OS Synthetic.  
 XX  
 PN US5631146-A.  
 XX  
 PD 20-MAY-1997.  
 XX  
 PF 19-JAN-1995; 95US-00375116.  
 XX  
 PR 19-JAN-1995; 95US-00375116.  
 XX  
 PA (GEHO) GEN HOSPITAL CORP.  
 XX  
 PI Szostak JM, Huizenga DE;  
 XX  
 DR WPI; 1997-288574/26.  
 XX  
 PT Single stranded DNA molecule, which binds adenosine or adenosine-5'-  
 PT phosphate - useful as purification reagent, or for determination of  
 PT adenosine triphosphate subcellular localization in vivo.  
 XX  
 PS Claim 3; Col 63-64; 55pp; English.  
 XX  
 CC The present sequence is an adenosine or adenosine-5'-phosphate (ASP)  
 CC binding single stranded DNA molecule, which can be used as a purification  
 CC reagent for the isolation of adenosine or an ASP, or to determine the  
 CC subcellular localization of, e.g. adenosine triphosphate (ATP), in vivo.  
 CC The DNA molecule was prepared by contacting DNA molecules having a region  
 CC of random sequence with adenosine or ASP (preferably ATP), isolating a  
 CC subpopulation by partitioning DNA molecules which specifically bind the  
 CC adenosine or ASP, amplifying the subpopulation in vitro and repeating the  
 CC process 4 times to obtain a single stranded DNA molecule capable of

CC binding adenosine or ASP, i.e. Systematic Evolution of Ligands by  
 CC Exponential enrichment (SELEX). Catalytic DNA produced using the method  
 CC can be used as in vitro or in vivo catalysts, or to detect the presence  
 CC of the ligand. They may also be used in assays to detect molecules  
 CC modified by the DNA, which are not themselves ligands, e.g. DNA  
 CC phosphorylated by a polynucleotide kinase catalyst. The DNA molecule has  
 CC significant advantages over ligand binding and catalytic RNA in terms of  
 CC stability and synthesis cost  
 CC  
 SQ Sequence 14 BP; 5 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 180 CTTCTCCGCTA 191  
 DB 13 CTTCTCCGCTA 2  
 RESULT 94  
 ID AAQ40305  
 AC AAQ40305 standard; cDNA; 15 BP.  
 XX AAQ40305;  
 DT 25-MAR-2003 (revised)  
 DT 10-AUG-1993 (first entry)  
 XX  
 DE Sequence of PCR primer oligo lambda-F for amplification of a fragment of  
 DE PTOM38 encoding glyceraldehyde-3-phosphate dehydrogenase (GPDH).  
 XX  
 KM Glyceraldehyde-3-phosphate dehydrogenase; inhibitor; antisense RNA;  
 KM fruit; ripening; se.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9307275-A1.  
 XX  
 PD 15-APR-1993.  
 XX  
 PF 01-OCT-1992; 92WO-GB001806.  
 XX  
 PR 03-OCT-1991; 91GB-00021074.  
 XX  
 PA (ICIL) IMPERIAL CHEM IND PLC.  
 XX  
 PI Bird CR, Grierson D, Ray JA, Schuch W;  
 XX  
 DR WPI; 1993-134464/16.  
 XX  
 PT DNA constructs for anti-sense inhibition of GPDH in plants - used to  
 PT modify ripening characteristics of climacteric fruit via inhibition of  
 PT respiration.  
 XX  
 PS Example; Fig 2; 22pp; English.  
 XX  
 CC The cDNA sequence is a fragment of cDNA for tomato cytosolic GPDH used in  
 CC a novel DNA construct under control of transcriptional initiation region  
 CC operative in plants. The construct is used to produce plants in which  
 CC GPDH expression is modified; in partic. the constructs produce antisense  
 CC RNA to down regulate expression. The transcriptional initiation region is  
 CC a constitutive promoter. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 246 CTCCTGGAGCCC 257  
 DB 3 CTCCTGGAGCCC 14

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RESULT 95
AAQ89599
ID AAQ89599 standard; DNA; 15 BP.
XX
AC AAQ89599;
XX
DT 06-NOV-1995 (first entry)
XX
DE Lambda-gt11 5' sequencing primer.
XX
KW Kappa-casein; milk protein; primer; polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN US5391497-A.
XX
PD 21-FEB-1995.
XX
PF 13-OCT-1992; 92US-00962569.
XX
PR 13-OCT-1992; 92US-00962569.
XX
PA (COLS ) UNIV COLORADO FOUND INC.
XX
PI Ham RG, Jeffers KF, Menon RS, Chang Y;
XX
DR WPI; 1995-160470/21.
DR P-PADB; AAR72697.
XX
PT DNA encoding human kappa-casein - used for the prodn. of large amts. of
PT highly purified kappa-casein milk protein for infant use.
XX
PS Example B; Col 11; 14pp; English.
XX
CC A commercial cDNA library prepd. in lambda gt11 from mRNA obtd. from
CC human breast tissue removed during the third trimester of pregnancy was
CC screened with rabbit anti-bovine kappa-casein cDNA. The cDNA insert of a
CC recombinant phage was amplified by PCR using the primer given in AAQ89599
CC (located 13-27 bp upstream of the EcoRI site of lambda gt11) and AAQ89600
CC (located 8-22 bp downstream of the EcoRI site)
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGCCC 257
DB      3 CTCCTGGAGCCC 14

RESULT 96
AAT32436
ID AAT32436 standard; DNA; 15 BP.
XX
AC AAT32436;
XX
DT 30-SEP-1996 (first entry)
XX
DE PCR primer lambda gt11 forward.
XX
KW Wasp; venom; neurotoxin; insecticide; biological control agent;
KW Lepidoptera; insect; Bracon hebetor; polymerase chain reaction; PCR;
KW primer; ss.
XX
OS Synthetic.
XX
PN WO9616171-A1.
XX
PD 30-MAY-1996.

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XX
PF 21-NOV-1995; 95WO-GB002720.
XX
PR 22-NOV-1994; 94GB-00023540.
PR 19-JAN-1995; 95GB-00001074.
PR 29-JUN-1995; 95GB-00013293.
XX
PA (ZENE ) ZENECA LTD.
PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX
PI Windass JD, Duncan RE, Baule VJ, Christian PD;
XX
DR WPI; 1996-268607/27.
XX
PT Bracon hebetor toxins and DNA encoding them - useful in biological
PT control agents to combat insect pests.
XX
PS Example 4; Page 20; 83pp; English.
XX
CC The PCR primer pair lambda gt11 forward (AAT32436) and lambda gt11
CC reverse (AAT32437) were used to screen for the presence of a cDNA insert
CC in plaque-purified phage obtd. from a Bracon hebetor wasp cDNA library.
CC The primers are specific for phage lambda gt11 and flank the EcoRI
CC cloning site. cDNA clone pBhtx-1(a)1.1 (AAT32438) was identified that
CC codes for the toxin (a) subunit (AAR99568) of the wasp neurotoxin Bhtx-
CC 1. This can be utilised in breeding of biological control agents used to
CC combat insect pests
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CTCCTGGAGCCC 257
DB      3 CTCCTGGAGCCC 14

RESULT 97
AA56935/C
ID AA56935 standard; DNA; 15 BP.
XX
AC AA56935;
XX
DT 16-OCT-2003 (revised)
DT 15-JUN-1999 (first entry)
XX
DE HIV-1 proviral DNA fragment 18.
XX
KW DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;
KW viral DNA-binding agent; solid support; primer; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9531434-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US006379.
XX
PR 13-MAY-1994; 94US-00242664.
XX
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
PA (ZWBI-) ZW BIOMEDICAL RES AG.
XX
PI Watanabe KA, Ren W, Weil R;
XX
DR WPI; 1996-010846/01.
XX
PT Derivatised solid supports and reagents for oligo:nucleotide synthesis -
PT and new oligo:nucleotide phosphoramidate conjugates.
XX

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PS Disclosure; Page 46; 68pp; English.

This invention describes novel derivatised solid supports of formula  $S'-L$ -Z-CH<sub>2</sub>CH<sub>2</sub>-R, where: S' = a solid support; L = a bond or an (in)organic linker; Z = SO<sub>2</sub> or S-S; R = OH, an H-phosphonate, alkane phosphonate, phosphorite, phosphite triester, phosphate diester, phosphorothioate, phosphorodithioate, phosphoramidate or phosphoramidite group, OR<sub>1</sub>, SR<sub>1</sub>, or an optionally substituted or modified nucleotide (N'), or an oligonucleotide of formula (N')<sub>g</sub>; g = 1-200; R<sub>1</sub> = a protecting group; R<sub>2</sub> = an H-phosphonate, alkane phosphonate, phosphorite, phosphite triester, phosphate diester, phosphorothioate, phosphorodithioate, phosphoramidate or phosphoramidite group, OH, OR<sub>1</sub>, SR<sub>1</sub> or OP(OCH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>NO)<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>OR<sub>1</sub>. Also mentioned are compounds of formula R<sub>3</sub>CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>CH<sub>2</sub>R<sub>4</sub>, where: R<sub>3</sub> = a protecting group; and R<sub>4</sub> = OH or an H-phosphonate, alkane phosphonate, phosphorite, phosphite triester, phosphate diester, phosphorothioate, phosphorodithioate, phosphoramidate or phosphoramidite group. Also claimed are new phosphoramidates, a process for preparing an oligonucleotide 5'-phosphate, a process for preparing a solid support useful for preparation of an oligonucleotide 3'-phosphate, a process for preparing an oligonucleotide 3'-phosphate and a process for preparing an oligonucleotide 3',5'-diphosphate. The oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNA-targeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNA-cleaving or -binding agents. The process for preparing oligonucleotide 3',5'-diphosphates is simple and suitable for use in automatic DNA synthesizers. This sequence represents a fragment of the HIV-1 provirus genome, used to describe the method of the invention. (Updated on 16-Oct-2003 to standardise OS field)

Sequence 15 BP; 9 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match	2.0%;	Score 12;	DB 2;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 1.2e+05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	175	TTGCTCTTCCTC	186
Db	13	TTGCTCTTCCTC	2

RESULT 98  
AAT14822  
ID AAT14822 standard; DNA; 15 BP.  
.....

AC AAT14822

DT 17-SEP-1996 (first entry)

Lambda gtl1 flanking sequence 5' primer.

Histiocyte-secreted factor; HSF; cytokine; antitumour; tumour; therapy;

XX Synthetic.

PN W09613586-A2.

PD 09-MAY-1996

26-OCT-1995; 95WO-JP002200.

PR 26-OCT-1994; 94JP-00297780.

PA (SATO/) SATOMI N

PI Satomi N;  
vv

DR WPI; 1996-239499/24.

PT DNA encoding histiocyte-secreted factor and its variants - useful as an

PT cytotoxicity compared to TNF.

PS Example 6; Page 30; 52pp; English.

CC lambda g11 5' (AATT14822) and 3' (AATT14823) primers were used in a lambda  
CC g11 cDNA insert screening kit to identify insert DNA in clones obt. by  
CC the PCR amplification of human histiocytic lymphoma DNA from a lambda  
CC g11 library. A genomic clone (AATT14818) coding for human HSP (AAR96800),  
CC a novel cytokine, was identified

SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match	2.0%;	Score 12;	DB 2;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 1.2e+05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	246	CTCCTGGAGCCC	257
Dib	3	CTCCTGGAGCCC	14

RESULT 99  
AAT35227  
ID AAT35227 standard; DNA; 15 BP

AC AAT35227;

DT 05-DEC-1996 (first entry)

Cytoplasmic antiproteinase PCR primer ZC2683.

KM Cytoplasmic antiproteinase-2 protein; CAP-2; CAP-3; serpin;  
KM serine protease inhibitor; antiinflammatory; apoptosis;  
KM polymerase chain reaction; PCR; primer; ss.

OS Synthetic.

PN W09624650-A2

PD 15-AUG-1996.

PF 02-FEB-1996; 96WO-US001288

PR 08-FEB-1995; 95US-00385

PA (ZYMO) ZYMO

PI Sprecher CA;

DR WPI; 1996-393014/39

PS Example 1; Page 43; 50pp; English.

**Sequence** 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match	2.0%;	Score 12;	DB 2;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 1.2e+05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	246	CTCCTGGAGCCC	257
Db	3	CTCCTGGAGCCC	14

```

RESULT 100
AAV17170
ID AAV17170 standard; DNA; 15 BP.
XX
AC AAV17170;
XX
AT 18-JUN-1998 (first entry)
XX
DE Insecticidal toxin subunit cDNA amplifying primer 1.
XX
KW Insecticidal toxin; Bracon hebetor; insect control; pathogen;
XX recombinant baculovirus; PCR primer; ss.
XX
OS Synthetic.
XX Bracon hebetor.
XX
PN WO9744355-A1.
XX
PD 27-NOV-1997.
XX
PF 01-MAY-1997; 97WO-GE001205.
XX
PR 22-MAY-1996; 96GB-00010687.
XX 22-MAY-1996; 96GB-00010695.
XX 22-MAY-1996; 96GB-00010697.
XX 22-MAY-1996; 96GB-00010738.
XX 22-MAY-1996; 96GB-00010739.
XX 22-MAY-1996; 96GB-00010748.
XX
PA (ZENE) ZENECA LTD.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Duncan RE, Suner M, Daly A, Christian PD, Windass JD,
PI Claudianos A;
XX
DR WPI; 1998-018430/02.
XX
PT New nucleic acid encoding a combination of insecticidal subunit(s) of
PT wasp toxin - and related transformed cells, insect pathogens and
PT combinations of proteins, useful as insecticides.
XX
PS Disclosure; Page 61; 84pp; English.
XX
CC This primer is used for PCR amplification of an insecticidal toxin
CC subunit cDNA of the invention. The specification provides a 1811 base
CC pair spliced RNA (AAV17183) derived from a Bracon hebetor genomic clone
CC that encodes at least two of the insecticidal toxin subunits shown in
CC sequences AAW52124-W52128. The spliced RNA can hybridise with extension
CC products prepared from a 564 base pair (AAV17145) template with 6
CC specified primers. A nucleic acid encoding at least one of the specified
CC subunits can be modified so that mRNA instability motifs and/or
CC fortuitous splice sites are removed, or insect-pest preference codons are
CC used, so that expression of this nucleic acid in insect cells yields
CC practically the same protein as unmodified nucleic acid in its endogenous
CC organism. The nucleic acid encoding an insecticidal toxin subunit can be
CC complementary to a sequence that hybridises under specified conditions to
CC any of sequences shown in AAV17145 to AAV17149. Cells transformed with
CC these nucleic acids, organisms regenerated from these cells and pathogens
CC containing these nucleic acids and insecticidal compositions comprising a
CC combinations of the toxin subunits are all used for control of insects.
CC The nucleic acids are used to produce recombinant baculoviruses for
CC insect control
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 257
DB 3 CTCCTGAGGCC 14

```

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RESULT 101
AAV15707
ID AAV15707 standard; DNA; 15 BP.
XX
AC AAV15707;
XX
AT 03-JUL-1998 (first entry)
XX
DE Primer for recombinant mosquito salivary allergen rae4 a 3 cDNA.
XX
KW Recombinant; mosquito; salivary allergen; rae4 a 3; determination;
XX bite sensitivity; epi-cutaneous test; skin test; intradermal test;
XX allergy diagnosis; immunotherapy; desensitisation; PCR primer; ss.
XX
OS Synthetic.
XX Aedes aegypti.
XX
PN WO9804274-A1.
XX
PD 05-FEB-1998.
XX
PF 31-JUL-1997; 97WO-US013573.
XX
PR 31-JUL-1996; 96US-0023118P.
XX
PA (UTMA-) UNITV MANITOBA.
XX (KOHN/) KOHN K I.
XX
PI Peng Z, Simons F;
XX
DR WPI; 1998-130418/12.
XX
PT Recombinant mosquito salivary allergens for use in skin tests for
PT sensitivity - also as substrate for assaying allergen-specific
PT immunoglobulin and for de-sensitisation immuno-therapy.
XX
PS Example 4; Page 43; 82pp; English.
XX
CC The present sequence is a primer for the cDNA encoding the recombinant
CC mosquito salivary allergen rae4 a 3. rae4 a 3 can be used to determine
CC sensitivity to mosquito bites by epi-cutaneous or intradermal testing, as
CC a substrate to which IgE/G bind (e.g. for mosquito allergy diagnosis) and
CC (based on the results of the skin tests) for immunotherapy
CC (desensitisation)
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 257
DB 3 CTCCTGAGGCC 14

```

```

OS Synthetic.
OS Aedes aegypti.
XX
XX MO925826-A1.
XX
XX 27-MAY-1999.
XX
XX 13-NOV-1998; 98WO-IB001961.
XX
XX 13-NOV-1997; 97US-0065402P.
XX
XX (UTMA-) UNIV MANITOBA.
XX
XX Simons FER, Peng Z;
XX
XX WPI; 1999-347473/29.
XX
XX Mosquito extract consisting of antigens to allergens in mosquito saliva.
XX
XX Example 4; Page 41; 77pp; English.
XX
XX The present invention describes a mosquito extract consisting essentially
XX of antigens related solely to allergens in mosquito saliva. The isolated
XX and purified recombinant mosquito salivary antigens are for use in skin
XX test, immunoassays and immunotherapy for allergic reactions to mosquito
XX bites. The mosquito extract consists essentially of these antigens to
XX allergens in mosquito saliva. The assays are applicable to patients
XX presenting with rashes and other symptoms after mosquito bites,
XX especially those with erythema, edema and induration, pain or itch at
XX the site(s) of mosquito bite(s), with or without fever. These patients
XX are at risk for severe localized inflammatory reactions and systemic
XX reactions to mosquito bites. The present sequence represents a PCR primer
XX for an Aed a 3 cDNA clone AA22, which was isolated from Aedes aegypti
XX (mosquito) saliva in an example from the present invention for the
XX isolation of a cDNA encoding a 30 kDa IGF-binding protein
XX
XX Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match
XX Best Local Similarity 2.0%; Score 12; DB 2; Length 15;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 246 CTCCTGGAGCCC 257
XX Db 3 CTCCTGGAGCCC 14
XX
XX RESULT 103
XX AA239756
XX ID AA239756 standard; DNA; 15 BP.
XX
XX AA239756;
XX
XX 06-MAR-2000 (first entry)
XX
XX Human CAP DNA specific primer ZC2683.
XX
XX Caspase; serpin; inflammation; apoptosis; lung disease; human; CAP;
XX neurodegenerative disease; heart; liver tissue; Alzheimer's disease;
XX Parkinson's disease; amyotrophic lateral sclerosis; injury; trauma;
XX hypoxia-ischaemia; cytoplasmic antiprotease protein; PCR primer;
XX nocrotropic; neuroprotective; vasotrophic; tranquilizer; vulnery; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9957273-A2.
XX
XX 11-NOV-1999.
XX
XX 27-APR-1999; 99WO-US008949.
XX
XX 04-MAY-1998; 98US-00072275.
XX

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XX
XX (ZYMO) ZYMOGENETICS.
XX
XX Sprechter CA, Foster DC, Jaepers SR;
XX
XX WPI; 2000-062146/05.
XX
XX Method for treating disease or symptoms of a disease mediated by a
XX caspase.
XX
XX Example 1; Page 63; 65pp; English.
XX
XX The invention provides a method for treating a disease mediated by a
XX caspase in an individual. The method comprises administering a
XX composition comprising a gene coding for an intracellular mammalian
XX serpin in an amount sufficient to inhibit activity of the caspase upon
XX transient expression of the gene in a target tissue affected by the
XX disease, where the disease or the symptoms are treated. The method can be
XX used for decreasing inflammation, for modulating apoptosis, for treating
XX a lung disease, and for treating a neurodegenerative disease. The
XX inflammation and apoptosis that can be treated are particularly in heart
XX or liver tissue. It can be used for treating Alzheimer's disease,
XX Parkinson's disease, amyotrophic lateral sclerosis, and acute injury such
XX as hypoxia-ischaemia or trauma. Sequences AA239755-56 represent PCR
XX primers specific for the human cytoplasmic antiprotease protein (CAP)
XX
XX Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match
XX Best Local Similarity 2.0%; Score 12; DB 3; Length 15;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 246 CTCCTGGAGCCC 257
XX Db 3 CTCCTGGAGCCC 14
XX
XX RESULT 104
XX AAH21253
XX ID AAH21253 standard; DNA; 15 BP.
XX
XX AAH21253;
XX
XX 13-SEP-2001 (first entry)
XX
XX Human Kv4.1 screening amplicon SEQ ID 10.
XX
XX Human, Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;
XX neurodegenerative disease; ischemia; stroke; Alzheimer's disease;
XX Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;
XX learning capacity; protein kinase activator; anti-arrhythmic; primer; ss.
XX
XX Homo sapiens.
XX
XX DE19963612-A1.
XX
XX 12-JUL-2001.
XX
XX 29-DEC-1999; 99DE-01063612.
XX
XX 29-DEC-1999; 99DE-01063612.
XX
XX (GENI-) FORSCHUNGSSELSCHAFT GENION MBH.
XX
XX WPI; 2001-426637/46.
XX
XX New potassium channel subunit proteins, useful for identifying and
XX testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological
XX agents.
XX
XX Example 2; Page 26; 50pp; German.
XX
XX This invention describes a novel potassium channel protein (1) that is
XX

```

CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium  
CC channels containing (I) are used to identify and test: (i) compounds for  
CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,  
CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac  
CC arrhythmia, or those that improve learning capacity and memory; and (ii)  
CC activators of protein kinases. Host cells that express (i) can identify  
CC agents that do not interact significantly with channels and control I<sub>to</sub>  
CC (a quickly activated transient current), so lack the side effects of  
CC known anti-arrhythmic agents. They also eliminate, or reduce, the need  
CC for testing on organ cultures

SO Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257  
DB 3 CTCCTGAGGCC 14

RESULT 105  
AAFS0004/c  
ID AAF50004 standard; DNA; 15 BP.

AC AAF50004;  
XX  
XX  
XX 30-MAR-2001 (first entry)  
DT  
DE IGF-1 oligonucleotide #964.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
XX hyperneovascular condition; hyperplasia; kidney disease;  
XX neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR.

XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia

SO Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376  
DB 13 AGCCCGAGGGGC 2

RESULT 106  
AAFS0002/c  
ID AAF50002 standard; DNA; 15 BP.

AC AAF50002;  
XX  
XX  
XX 30-MAR-2001 (first entry)  
DT  
DE IGF-1 oligonucleotide #962.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;  
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;  
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;  
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
XX hyperneovascular condition; hyperplasia; kidney disease;  
XX neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR.

XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
PT inhibits or reduces growth factor mediated cell proliferation and/or  
PT inflammation.

XX Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC F45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC disease, kidney disease, hyperproliferation of the inside of blood  
vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376

Db 15 AGCCCGAGGGGC 4

RESULT 107

AAFS0003/c

ID AAF50003 standard; DNA; 15 BP.

AC AAF50003;

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #963.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
XX cytoskeletal; dermatological; cardiant; vitruide; ophthalmological; keloid;  
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
XX hyperneovascular condition; hyperplasia; kidney disease;  
XX neovascular condition of the retina; ss.

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000MO-AU000693.

PR 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
inhibits or reduces growth factor mediated cell proliferation and/or  
inflammation.

PS Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC P45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia

XX Sequence 15 BP; 0 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376

Db 14 AGCCCGAGGGGC 3

RESULT 108

AAFS0005/c

ID AAF50005 standard; DNA; 15 BP.

AC AAF50005;

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #965.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;  
XX cytoskeletal; dermatological; cardiant; vitruide; ophthalmological; keloid;  
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;  
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;  
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;  
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;  
XX hyperneovascular condition; hyperplasia; kidney disease;  
XX neovascular condition of the retina; ss.

OS Homo sapiens.

PN WO200078341-A1.

PD 28-DEC-2000.

PF 21-JUN-2000; 2000MO-AU000693.

PR 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

PI Wraight CJ, Werther GA, Edmondson SR;

DR WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering  
UV (ultra-violet) treatment (optional) and an antisense nucleic acid that  
inhibits or reduces growth factor mediated cell proliferation and/or  
inflammation.

PS Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of  
CC skin disorders. The method comprises contacting the skin with an  
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1  
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of  
CC inhibiting or reducing growth factor mediated cell proliferation,  
CC inflammation and/or other disorders. The present sequence is an  
CC oligonucleotide which can be used to design the antisense  
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-  
CC P45161). The method is useful for ameliorating the effects of psoriasis,  
CC ichthyosis, ptyriasis, ruba, pilaris, serborrhoea, keloids, keratosis,  
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a  
CC hyperneovascular condition such as a neovascular condition of the retina,  
CC brain or skin, growth factor-mediated malignancies, other sclerotic  
CC disease, kidney disease, hyperproliferation of the inside of blood  
CC vessels or any other hyperplasia

XX Sequence 15 BP; 1 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376  
 |||||  
 DB 12 AGCCCGAGGGGC 1

## RESULT 109

ACD26289  
 ID ACD26289 standard; DNA; 15 BP.

AC ACD26289;  
 XX

DT 03-SEP-2003 (first entry)

DE Gene chip associated oligonucleotide #1.

XX Gene chip; ss; hairpin; full match; single-point mismatch.

OS Unidentified.

XX CN1373228-A.  
 XX

PD 09-OCT-2002.  
 XX

PF 22-MAR-2002; 2002CN-00116302.

XX 22-MAR-2002; 2002CN-00116302.

XX (UYBE-) UNIV BEIJING.

XX Zhao X, Wei F, Sun B;  
 XX

DR WPI; 2003-141480/14.

PT Gene chip for recognizing full match and single-point mismatch, comprises  
 PT hairpin-shaped probes having a detecting region and a stem region.

PS Disclosure; Page 6 (Disclosure); 11pp; Chinese.

XX The invention relates to a gene chip which is composed of a chip  
 CC substrate and oligomeric nucleic acid probes fixed on the substrate. The  
 CC probe is composed of a detecting region and a stem region, where a  
 CC hairpin-shaped dual-chain structure is formed by the oligomeric nucleic  
 CC acid sequence and the one matched with it. Controlling the electric  
 CC potential of the gene chip can further optimize hybridisation conditions.  
 CC Its advantages are repeated application, low cost and the power for  
 CC recognizing full match and single-point mismatch. The present sequence  
 CC represents the gene chip associated oligonucleotide #1

XX Sequence 15 BP; 4 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGAGG 27  
 |||||

DB 4 ATGACCGAGG 15

## RESULT 110

AAQ6708/c  
 ID AAQ6708 standard; DNA; 16 BP.

XX AAQ6708;  
 AC

DT 22-DEC-1994 (first entry)

XX Primer to amplify HHV6 derived sequences.

DE HHV6; Human Herpes Virus 6; Primers; Probes; PCR; amplify;  
 XX polymerase chain reaction; ss.  
 XX

OS Synthetic.

XX JP06133799-A.  
 XX

PD 17-MAY-1994.  
 XX

PF 27-OCT-1992; 92JP-00311416.

XX 27-OCT-1992; 92JP-00311416.

XX (KOKU-) KOKUSAI SHIYAKU KK.  
 XX

DR WPI; 1994-196175/24.

XX HHV-6 derived nucleotide(s) - useful for identification of HHV-6 DNA.

XX Claim 4; Page 2; 13pp; Japanese.

CC The inventors provide human Herpes virus 6 derived nucleotide sequences  
 CC useful for identification of HHV-6 DNA. AAQ6705-12 are primer set 1 (1),  
 CC are used in the invention

XX Sequence 16 BP; 5 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 CATGAAATTC A 507  
 |||||

DB 12 CATGAAATTC A 1

## RESULT 111

ACA58181/c  
 ID ACA58181 standard; DNA; 16 BP.

XX ACA58181;  
 AC

DT 09-JUN-2003 (first entry)

XX Human familial bipolar affective disorder chromosome marker #129.

XX Human; genotype determination; familial bipolar affective disorder;  
 XX chromosomal region linked; locus associated with resistance; D4S402;  
 XX D4S42; D4S431; D4S404; D1S394; D1S29; chromosome marker; primer; ss.

XX Homo sapiens.

OS

XX US2002192655-A1.

XX 19-DEC-2002.

XX 13-JUN-2001; 2001US-00881012.

XX 29-MAR-1996; 96US-0014334P.

XX 20-OCT-1997; 97US-0062924P.

XX 19-OCT-1998; 98US-00175158.

XX (GINN/) GINN E I.  
 XX (EGEL/) EGELAND J A.  
 XX (PAUL/) PAUL S M.

XX Ginn EI, Egeland JA, Paul SM;  
 XX

DR WPI; 2003-352708/33.

PT Determining a genotype associated with increased or decreased resistance  
 PT to familial bipolar affective disorder in a family comprises determining  
 PT the genotype of e.g., chromosomal regions D4S402 and D4S424.  
 PS Disclosure; Page 11; 79pp; English.  
 XX



Db 1 ACCTCTGTGAGC 12

## RESULT 114

AA092156 standard; DNA; 17 BP.

AA092156;

11-JUN-1996 (first entry)

p53 detection probe, (codon 245 GGC to TGC).

Primer: polymerase chain reaction; amplify; mutant; K-ras; PCR;

flanking region; amplification; probe; detection; sputum; diagnosis;

benign; malignant; neoplasm; lung; lung cancer; head; neck; ss.

Synthetic.

MO9513397-A1.

18-MAY-1995.

10-NOV-1994; 94MO-US012947.

12-NOV-1993; 93US-00152313.

(UYUO) UNIV JOHNS HOPKINS SCHOOL MED.

Sidransky D;

WPI; 1995-194114/25.

Detecting target nucleic acid in mammalian sputum - particularly for

diagnosis of lung neoplasia involving mutation(s) in the K-ras oncogene

or p53 tumour suppressor.

Example 1; Page 32; 122pp; English.

The sequences given in AA092112-211 are probes which were used in the

detection of a mutant p53 gene sequence. The DNA to be detected is

amplified using PCR and then these probes which are pref. labeled using

32-P gamma-ATP are used to detect the mutant sequences. The primers and

probes given in AA092098-219 are used in the method of the invention for

detecting mammalian target DNA in sputum samples. Analysis of the target

DNA is used to diagnose benign or malignant neoplasms of the lung. It is

also useful for screening people at high risk or for monitoring progress

-of treatment for lung neoplasms. The method is based on the discovery that

mutant target DNA associated with lung cancer is present at detectable

levels in sputum. Cells shed into sputum from head and neck cancers may

also be detected

Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;

hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;

autoimmune disease; psoriasis; allergy; inflammatory disease;

graft rejection; ss.

Synthetic.

Canis sp.

MO9824913-A2.

11-JUN-1998.

02-DEC-1997; 97MO-US021748.

03-DEC-1996; 96US-00758306.

(RIBO-) RIBOZYME PHARM INC.

Stinchcomb DT, Mcswiggen JA;

WPI; 1998-333332/23.

Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,

autoimmune disease and allergies.

Claim 4; Page 47; 61pp; English.

The present sequence invention describes ribozymes targeted to modulate

the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.

AAV93889 to AAV94574 represent specifically claimed ribozymes, and

AAV94575 to AAV95260 represent specifically claimed substrate sequences

from the present invention. The ribozymes can be used for the treatment

of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy

and other inflammatory conditions. The ribozymes are also used to induce

tolerance in a recipient to alloantigen from a donor

Sequence 17 BP; 3 A; 3 C; 10 G; 0 T; 1 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

248 CCTGAGCCCT 259

13 CCTGAGCCCT 2

AA018564/c

AA018564 standard; RNA; 17 BP.

AA018564;

19-JUN-2000 (first entry)

Human TIE-2 substrate sequence SEQ ID NO:1790.

Human; aryl hydrocarbon nuclear transport; ANNT; TIE-2; angiogenesis;

integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;

ophthalmologic; antiinflammatory; antiaesthetic; antipruritic; ARMD;

dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;

age related macular degeneration; inflammation; neovascular glaucoma;

myopic degeneration; psoriasis; verruca vulgaris; angiodioma;

tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;

Kippel-Trennauy-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

Homo sapiens.

MO9950403-A2.

07-OCT-1999.

```

XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA,
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 56; Page 103; 305pp; English.
XX
XX The present invention describes enzymatic cleave RNA molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT.
XX Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 249 CTGGAGCCCCCTG 260
XX |||||
XX 12 CTGGAGCCCCCTG 1
XX
XX RESULT 117
XX AAA20707
XX ID AAA20707 standard; RNA; 17 BP.
XX
XX AAA20707;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3933.
XX
XX Human; aryl hydrocarbon nuclear transporter; ARNT, Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX

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OS Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA,
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 56; Page 162; 305pp; English.
XX
XX The present invention describes enzymatic cleave RNA molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT.
XX Integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 5 A; 4 C; 0 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 58.3%; Pred. No. 1.2e+05;
XX Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX 35 TTATCAATTC 46
XX ::|||
XX 6 TTTACCAATTC 17
XX
XX RESULT 118
XX AAV91124/c
XX ID AAV91124 standard; RNA; 17 BP.
XX
XX AAV91124;
XX
XX 18-FEB-1999 (first entry)
XX
XX Human C-raf target site nucleotide position 1289.
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalytic; modulation; expression; Raf gene; delivery;
XX screening; identification; synthesis; deprotection; purification; cancer;
XX inflammation; psoriasis; non-hepatic alectes; infection; genetic drift;
XX restenosis; rheumatoid arthritis; ss.
XX

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XX OS Homo sapiens.
XX PN MO9850530-A2.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US009249.
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kistich K, Bellon L;
PI Parry T, Beigelman L, Mcswigen JA, Karpetsky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX WPI; 1999-009494/01.
XX PT Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthonis.
XX PS Claim 177; Page 149; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC acetosis and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-rat RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-rat. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SO Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 170 TGGATTGCTCT 181
XX DB 12 TGGATTGCTCT 1
XX
XX RESULT 119
XX ID AAA36309 standard; DNA; 17 BP.
XX AC AAA36309;
XX XX
XX DT 26-JUL-2000 (first entry)
XX DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:375.

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XX OS Homo sapiens.
XX PN MO200018960-A2.
XX PD 06-APR-2000.
XX PF 24-SEP-1999; 99WO-US022283.
XX PR 25-SEP-1998; 98US-0101757P.
XX PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
XX PI Landers JE, Jordan B, Housman DE, Charest A;
XX WPI; 2000-293181/25.
XX PT Detection of single nucleotide polymorphisms in genomes by preparation
XX PT and analysis of reduced complexity genomes, useful for genotyping,
XX PT fingerprinting and determining allele frequency of SNPs.
XX PS Disclosure; Page 64; 11pp; English.
XX CC A method has been developed for detecting the presence or absence of a
XX CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX CC method comprises preparing a reduced complexity genome (RCG) from the
XX CC genomic sample and analyzing the RCG for the presence or absence of a SNP
XX CC allele. The method can be used to characterize a tumour, to generate a
XX CC genomic pattern for an individual genome or to generate a genomic
XX CC classification code for a genome. The method can be used to assess
XX CC whether a subject is at risk for developing a disease or to identify a
XX CC set of SNP alleles associated with a disease. The method can also be used
XX CC to perform linkage analysis. AAA35944 to AAA35947 represent sequences
XX CC used in the exemplification of the present invention. AAA35948 to
XX CC AAA36632 represent nucleotide sequences containing SNPs
XX SO Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 409 GCCATCATGACC 420
XX DB 5 GCCATCATGACC 16
XX
XX RESULT 120
XX ID AA288059 standard; DNA; 17 BP.
XX AC AA288059;
XX XX
XX DT 06-AUG-2003 (revised)
XX DT 20-APR-2000 (first entry)
XX DE Lentiviral proviral long terminal repeat DNA PCR primer #1.
XX KW Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX KW gene expression; PCR primer; ss.
XX OS Retroviridae.
XX PN WO200000600-A2.
XX XX
XX DT 06-JAN-2000.
XX DE 26-MAY-1999; 99WO-US011516.

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XX 26-MAY-1998; 98US-0086635P.
XX (CHAN/) CHANG L.
XX Chang L;
XX WPI; 2000-137067/12.
XX
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example; Page 132; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
XX lentivirus that differs from the reference lentivirus at least in that:
XX (a) its major splice donor site is either deleted or is insufficiently
XX different from the reference lentivirus so that it is not a potential
XX site for homologous recombination; and (b) it lacks a functional major
XX packaging signal so that the introduced vector causes the host cell to
XX produce packaging vector particles comprising functional Gag and Pol
XX proteins. The vectors are useful for transforming (eukaryotic) cells to
XX express specific genes at high levels, e.g. for gene therapy. The
XX improved vectors are safer, yet permit increased efficiency of packaging
XX the recombinant viral genome and increased long-term gene expression.
XX These properties are required for gene therapy as a means of treating
XX infectious and non-infectious diseases. Unlike other retroviruses, the
XX lentiviruses are able to infect non-dividing cells. The present sequence
XX represents a lentiviral proviral long terminal repeat DNA PCR primer
XX which is used in the exemplification of the present invention. (Updated
XX on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 246 CTCCTGAGGCC 257
XX |||||
XX 5 CTCCTGAGGCC 16
XX
XX Db
XX
XX RESULT 121
XX ID AA288115 standard; DNA; 17 BP.
XX AC AA288115;
XX DT 20-APR-2000 (first entry)
XX DE Hirt DNA PCR primer #1.
XX KM Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX KM gene expression; PCR primer; ss.
XX OS Synthetic.
XX PN WO200000600-A2.
XX PD 06-JAN-2000.
XX PF 26-MAY-1999; 99WO-US011516.
XX PR 26-MAY-1998; 98US-0086635P.
XX PA (CHAN/) CHANG L.
XX PI Chang L;
XX WPI; 2000-137067/12.
XX
```

```
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example 200; Page 213; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
XX lentivirus that differs from the reference lentivirus at least in that:
XX (a) its major splice donor site is either deleted or is insufficiently
XX different from the reference lentivirus so that it is not a potential
XX site for homologous recombination; and (b) it lacks a functional major
XX packaging signal so that the introduced vector causes the host cell to
XX produce packaging vector particles comprising functional Gag and Pol
XX proteins. The vectors are useful for transforming (eukaryotic) cells to
XX express specific genes at high levels, e.g. for gene therapy. The
XX improved vectors are safer, yet permit increased efficiency of packaging
XX the recombinant viral genome and increased long-term gene expression.
XX These properties are required for gene therapy as a means of treating
XX infectious and non-infectious diseases. Unlike other retroviruses, the
XX lentiviruses are able to infect non-dividing cells. The present sequence
XX represents an oligonucleotide which is used in the exemplification of the
XX present invention
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX QY 246 CTCCTGAGGCC 257
XX |||||
XX 5 CTCCTGAGGCC 16
XX
XX Db
XX
XX RESULT 122
XX ID AA288064 standard; DNA; 17 BP.
XX AC AA288064;
XX DT 20-APR-2000 (first entry)
XX DE MLV proviral long terminal repeat DNA PCR primer #2.
XX KM Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX KM gene expression; PCR primer; ss.
XX OS Murine leukemia virus.
XX PN WO200000600-A2.
XX PD 06-JAN-2000.
XX PF 26-MAY-1999; 99WO-US011516.
XX PR 26-MAY-1998; 98US-0086635P.
XX PA (CHAN/) CHANG L.
XX PI Chang L;
XX WPI; 2000-137067/12.
XX
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example; Page 132; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
```



OS Synthetic.  
 XX  
 PN MO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 88; Page 66; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is a hammerhead ribozyme of the invention  
 XX  
 SQ Sequence 17 BP; 1 A; 6 C; 7 G; 0 T; 3 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 362 CTGAGCCCGAGG 373  
 DB 17 CTGAGCCCGAGG 6

ID ABK00947 standard; RNA; 17 BP.  
 XX  
 AC ABK00947;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Inozyme #217.  
 XX  
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;  
 KW cerebroprotective; neuroprotective; antiparkinsonian;  
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukemia;  
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;  
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;  
 KW inflammatory arthropathy; central nervous system injury;  
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KW Parkinson's disease; ataxia; Huntington's disease;  
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001WO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM;  
 XX  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 88; Page 81; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an inozyme of the invention

XX Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Qy Query Match 2.0%; Score 12; DB 4; Length 17;  
 Db Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 CTGAGCCCGAGG 373  
 Db 12 CTGAGCCCGAGG 1

RESULT 126  
 ID ABR02420 standard; RNA; 17 BP.  
 AC ABR02420;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Amberzyme #92.  
 XX  
 XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
 KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KM DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KM inflammatory arthropathy; central nervous system injury;  
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KM Parkinson's disease; ataxia; Huntington's disease;  
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001MO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT) BLATT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BM,  
 DR WPI, 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 XX Claim 88; Page 132; 200pp; English.  
 PS  
 XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a  
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA  
 CC with a YG motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-  
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOGO. The treatment may further comprise the use of one or more  
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOGO expression. The present  
 CC sequence is an amberzyme molecule of the invention

XX Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Qy Query Match 2.0%; Score 12; DB 4; Length 17;  
 Db Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 CTGAGCCCGAGG 373  
 Db 16 CTGAGCCCGAGG 5

RESULT 127  
 ID ABR01846 standard; RNA; 17 BP.  
 AC ABR01846;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human NOGO Zinczyme #168.  
 XX  
 PF 09-FEB-2001; 2001MO-US004273.  
 XX  
 PR 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;  
 KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;  
 KM DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;  
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;  
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;  
 KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;  
 KM inflammatory arthropathy; central nervous system injury;  
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;  
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;  
 KM Parkinson's disease; ataxia; Huntington's disease;  
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200159103-A2.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 09-FEB-2001; 2001MO-US004273.

XX 11-FEB-2000; 2000US-0181797P.  
 PR 28-FEB-2000; 2000US-0185516P.  
 PR 06-MAR-2000; 2000US-0187128P.  
 XX  
 XX (RIBO-) RIBOZYME PHARM INC.  
 PA (BLAT/) BLAT L.  
 PA (MCSW/) MCSWIGGEN J.  
 PA (CHOW/) CHOWRIRA B M.  
 XX  
 PI Blatt L, Mcswiggen J, Chowrira BW,  
 DR WPI; 2001-607195/69.  
 XX  
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense  
 PT constructs, which down regulate expression of a CD20 gene or neurite  
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and  
 PT central nervous system injury.  
 XX  
 PS Claim 88; Page 98; 200pp; English.  
 XX  
 CC The invention relates to a nucleic acid molecule which down regulates  
 CC expression of a CD20 gene and a nucleic acid molecule which down  
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The  
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a  
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule  
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or  
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA  
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA  
 CC of CD20 in the presence of a divalent cation that is preferably Mg<sup>2+</sup>.  
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of  
 CC the cell and treat a patient having a condition associated with the level  
 CC of CD20. The treatment may further comprise the use of one or more  
 CC therapias. In particular, the CD20 targeting nucleic acid may be used to  
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-  
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic  
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell  
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,  
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-  
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the  
 CC presence of a divalent cation that is preferably Mg<sup>2+</sup>. Furthermore, the  
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the  
 CC cell and treat a patient having a condition associated with the level of  
 CC NOCO. The treatment may further comprise the use of one or more  
 CC therapias. In particular, the NOCO-targeting nucleic acid may be used to  
 CC treat central nervous system (CNS) injury and cerebrovascular accident  
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),  
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),  
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob  
 CC disease, muscular dystrophy, and/or other neurodegenerative disease  
 CC states which respond to the modulation of NOCO expression. The present  
 CC sequence is a zinzyme molecule of the invention  
 XX  
 SO Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 362 CTGAGCCCGAGG 373  
 DB 14 CTGAGCCCGAGG 3  
 RESULT 128  
 ID ABA77345 standard; DNA; 17 BP.  
 XX ABA77345;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 XX p53 mutation correcting oligonucleotide SEQ ID NO: 191.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KW retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;  
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thromboside;  
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KW Alzheimer's disease; cytosolic; antisticking; antineutrophilic; haemostatic;  
 KW antileptemic; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX W0200173002-A2.  
 PN  
 XX 04-OCT-2001.  
 PD  
 XX 27-MAR-2001; 2001WO-US009761.  
 PF  
 XX 27-MAR-2000; 2000US-0192176P.  
 PR 27-MAR-2000; 2000US-0192176P.  
 PR 01-JUN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 PI Kmiec EB, Gamper HB, Rice MC;  
 PI WPI; 2001-639230/73.  
 DR  
 XX  
 XX Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical  
 PT modification.  
 XX  
 PS Claim 7; Page 54; 294pp; English.  
 XX  
 CC The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SO Sequence 17 BP; 5 A; 6 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 ATGAACCGGAGG 27  
 DB 2 ATGAACCGGAGG 13  
 RESULT 129  
 ID ABA77317 standard; DNA; 17 BP.  
 XX ABA77317;  
 XX  
 XX 24-JAN-2002 (first entry)  
 DT  
 XX

DE p53 mutation correcting oligonucleotide SEQ ID NO: 163.  
XX  
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
KM retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;  
KM cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
KM adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
KM haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;  
KM mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
KM familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
KM UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
KM Alzheimer's disease; cytoskeletal; antitickling; antianemic; haemostatic;  
KM antileptic; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO2001.73002-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX  
XX 27-MAR-2001; 2001WO-US009761.  
PF  
XX  
XX 27-MAR-2000; 2000US-0192176P.  
PR  
XX 27-MAR-2000; 2000US-0192179P.  
PR  
XX 01-JUN-2000; 2000US-0208538P.  
PR  
XX 30-OCT-2000; 2000US-0244989P.  
XX  
XX (UYDE ) UNIV DELAWARE.  
PA  
XX Kmiec EB, Gamper HB, Rice MC;  
PI  
XX WPI; 2001-639230/73.  
DR  
XX  
XX Oligonucleotide for targeted alterations of genetic sequences and for  
PT treating cystic fibrosis, comprises at least one mismatch and chemical  
PT modification.  
PT  
XX  
XX Claim 7; Page 51; 294pp; English.  
XX  
XX The present invention provides single-stranded oligonucleotides which can  
CC be used for the targeted alteration of genomic sequences, where the  
CC oligonucleotide has at least one mismatch compared with the genomic  
CC sequence to be altered. In particular, these sequences are directed at  
CC the following genes: adenosine deaminase, p53, beta-globin,  
CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A  
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,  
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
CC various syndromes. The present sequence is one of the gene correcting  
CC oligonucleotides of the invention  
XX  
XX Sequence 17 BP; 4 A; 6 C; 6 G; 1 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 2.0%; Score 12; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 ATGAACCGGAGG 27  
DB 3 ATGAACCGGAGG 14

XX  
XX p53 mutation correcting oligonucleotide SEQ ID NO: 164.  
DE  
XX  
XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
KM retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;  
KM cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
KM adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
KM haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;  
KM mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
KM familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
KM UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
KM Alzheimer's disease; cytoskeletal; antitickling; antianemic; haemostatic;  
KM antileptic; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO2001.73002-A2.  
PN  
XX 04-OCT-2001.  
PD  
XX  
XX 27-MAR-2001; 2001WO-US009761.  
PF  
XX  
XX 27-MAR-2000; 2000US-0192176P.  
PR  
XX 27-MAR-2000; 2000US-0192179P.  
PR  
XX 01-JUN-2000; 2000US-0208538P.  
PR  
XX 30-OCT-2000; 2000US-0244989P.  
XX  
XX (UYDE ) UNIV DELAWARE.  
PA  
XX Kmiec EB, Gamper HB, Rice MC;  
PI  
XX WPI; 2001-639230/73.  
DR  
XX  
XX Oligonucleotide for targeted alterations of genetic sequences and for  
PT treating cystic fibrosis, comprises at least one mismatch and chemical  
PT modification.  
PT  
XX  
XX Claim 7; Page 52; 294pp; English.  
XX  
XX The present invention provides single-stranded oligonucleotides which can  
CC be used for the targeted alteration of genomic sequences, where the  
CC oligonucleotide has at least one mismatch compared with the genomic  
CC sequence to be altered. In particular, these sequences are directed at  
CC the following genes: adenosine deaminase, p53, beta-globin,  
CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A  
CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and  
CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases  
CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,  
CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
CC various syndromes. The present sequence is one of the gene correcting  
CC oligonucleotides of the invention  
XX  
XX Sequence 17 BP; 1 A; 6 C; 6 G; 4 T; 0 U; 0 Other;  
SQ  
XX  
XX Query Match 2.0%; Score 12; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 ATGAACCGGAGG 27  
DB 15 ATGAACCGGAGG 4

RESULT 130  
ABAT77318/C  
ID ABA77318 standard; DNA; 17 BP.  
XX  
XX ABA77318;  
AC  
XX  
DT 24-JAN-2002 (first entry)

RESULT 131  
ABAT77346/C  
ID ABA77346 standard; DNA; 17 BP.  
XX  
XX ABA77346;  
AC  
XX

DT 24-JAN-2002 (first entry)  
 XX  
 DE P53 mutation correcting oligonucleotide SEQ ID NO: 192.  
 XX  
 KM Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;  
 KM retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;  
 KM cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;  
 KM adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;  
 KM haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;  
 KM muscle repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;  
 KM familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;  
 KM UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;  
 KM Alzheimer's disease; cyclostatic; antitickling; antianemic; haemostatic;  
 KM antileptic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200173002-A2.  
 XX  
 PD 04-OCT-2001.  
 XX  
 PF 27-MAR-2001; 2001WO-US009761.  
 XX  
 PR 27-MAR-2000; 2000US-0192176P.  
 XX  
 PR 27-MAR-2000; 2000US-0192179P.  
 PR 01-UTN-2000; 2000US-0208538P.  
 PR 30-OCT-2000; 2000US-0244989P.  
 XX  
 PA (UYDE ) UNIV DELAWARE.  
 XX  
 PI Kmiec EB, Gampier HB, Rice MC;  
 XX  
 DR WPI; 2001-639230/73.  
 XX  
 PT Oligonucleotide for targeted alterations of genetic sequences and for  
 PT treating cystic fibrosis, comprises at least one mismatch and chemical  
 PT modification.  
 XX  
 PS Claim 7; Page 54; 294pp; English.  
 XX  
 CC The present invention provides single-stranded oligonucleotides which can  
 CC be used for the targeted alteration of genomic sequences, where the  
 CC oligonucleotide has at least one mismatch compared with the genomic  
 CC sequence to be altered. In particular, these sequences are directed at  
 CC the following genes: adenosine deaminase, p53, beta-globin,  
 CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A  
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus  
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,  
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase  
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and  
 CC presenilin-2 (PSN2). These can be used in the gene therapy of diseases  
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,  
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,  
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and  
 CC various syndromes. The present sequence is one of the gene correcting  
 CC oligonucleotides of the invention  
 XX  
 SO Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.0%; Score 12; DB 4; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 DB Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 16 ATGAACCGAGG 27  
 16 ATGAACCGAGG 5

XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7365.  
 XX  
 KM Human; genome-derived myosin-like protein 1; GDMLP-1; heart;  
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KM skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AECM-) AECOMICA INC.  
 XX  
 PI Gu Y, Yi Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX  
 DR WPI; 2002-179446/23.  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption/ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 7365; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SO Sequence 17 BP; 7 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 2.0%; Score 12; DB 6; Length 17;  
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510  
 |||||  
 Db 5 GAAATTCAGTT 16

RESULT 133  
 ABN07376  
 ID ABN07376 standard; DNA; 17 BP.  
 XX  
 AC ABN07376;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMPL-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7368.  
 XX  
 KM Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;  
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KM skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200192524-A2.  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0268660P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 DR WPI; 2002-179446/23.  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPL-1.  
 XX  
 PS Disclosure; SEQ ID NO 7368; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPL-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMPL  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMPL proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption/ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMPL-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMPL-1, in particular heart  
 CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 8 A; 1 C; 3 G; 5 T; 0 U; 0 Other;  
 XX

Query Match 2.0%; Score 12; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510  
 |||||  
 Db 2 GAAATTCAGTT 13

RESULT 134  
 ABN07375  
 ID ABN07375 standard; DNA; 17 BP.  
 XX  
 AC ABN07375;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMPL-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7367.  
 XX  
 KM Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;  
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KM skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200192524-A2.  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0268660P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 DR WPI; 2002-179446/23.  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMPL-1.  
 XX  
 PS Disclosure; SEQ ID NO 7367; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1  
 CC nucleic acids can be used as probes to detect, characterise and quantify  
 CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMPL-1



PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 7364; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterize and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 T; 0 U; 0 Other;  
 XX  
 SQ  
 CC Query Match 2.0%; Score 12; DB 6; Length 17;  
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 499 GAAATTCACTT 510  
 DB 6 GAAATTCACTT 17  
 XX  
 RESULT 137  
 ABN07374  
 ID ABN07374 standard; DNA; 17 BP.  
 XX  
 AC ABN07374;  
 XX  
 DT 29-MAY-2002 (first entry)  
 XX  
 DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7366.  
 XX  
 KM Human; genome-derived myosin-like protein 1; GDMLP-1; heart;  
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;  
 KM skeletal muscle disorder; amplicon; screening; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200192524-A2.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 25-MAY-2001; 2001WO-US016981.  
 XX  
 PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 PR 30-JAN-2001; 2001WO-US000661.  
 PR 30-JAN-2001; 2001WO-US000662.  
 PR 30-JAN-2001; 2001WO-US000663.  
 PR 30-JAN-2001; 2001WO-US000664.  
 PR 30-JAN-2001; 2001WO-US000665.  
 PR 30-JAN-2001; 2001WO-US000666.  
 PR 30-JAN-2001; 2001WO-US000667.  
 PR 30-JAN-2001; 2001WO-US000668.  
 PR 30-JAN-2001; 2001WO-US000669.  
 PR 30-JAN-2001; 2001WO-US000670.  
 PR 05-FEB-2001; 2001US-0266860P.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;  
 XX WPI; 2002-179446/23.  
 DR  
 XX  
 PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,  
 PT or as specific biomolecule capture probes for surface-enhanced laser  
 PT desorption ionization, comprises human myosin-like protein hGDMLP-1.  
 XX  
 PS Disclosure; SEQ ID NO 7366; 214pp; English.  
 XX  
 CC The present invention describes a human genome-derived myosin-like  
 CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-  
 CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1  
 CC nucleic acids can be used as probes to detect, characterize and quantify  
 CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to  
 CC provide initial substrates for the recombinant engineering of hGDMLP-1  
 CC protein variants having desired phenotypic improvements, and for  
 CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be  
 CC used as immunogens to raise antibodies that specifically recognise hGDMLP  
 CC -1 proteins, as standards in assays used to determine the concentration  
 CC and/or amount specifically of hGDMLP proteins, as specific biomolecule  
 CC capture probes for surface-enhanced laser desorption ionization, as  
 CC therapeutic supplement in patients having specific deficiency in hGDMLP-1  
 CC production, and in vaccines or for replacement therapy. The  
 CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a  
 CC disorder associated with the expression of hGDMLP-1, in particular heart  
 CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.  
 CC The present sequence represents an oligomer used in the screening of the  
 CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequence  
 XX  
 SQ Sequence 17 BP; 7 A; 2 C; 4 G; 4 T; 0 U; 0 Other;  
 XX  
 SQ  
 CC Query Match 2.0%; Score 12; DB 6; Length 17;  
 CC Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 499 GAAATTCACTT 510  
 DB 4 GAAATTCACTT 15  
 XX  
 RESULT 138  
 ABV85812  
 ID ABV85812 standard; DNA; 17 BP.  
 XX  
 AC ABV85812;  
 XX  
 DT 11-DEC-2002 (first entry)  
 XX  
 DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:805.  
 XX  
 KM Human; UDP-GalNAc:polypeptide N-acetylglactosaminyltransferase 10;  
 KM pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;  
 KM

```

KM ss.
XX Homo sapiens.
OS Synthetic.
XX EP1243660-A2.
XX
XX 25-SEP-2002.
XX
XX 25-JAN-2002; 2002EP-00001161.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX and treat disorders associated with reduced or over expression of the
XX encoded protein.
XX
XX Example 2; SEQ ID NO 805; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
XX human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
XX chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX present invention can be used in therapy, particularly to prevent or
XX treat a disorder associated with decreased expression or activity of pp-
XX GaNTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
XX ABP53504 are given in the exemplification of the present invention. N.B.
XX The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied by the
XX European Patent Office
XX
XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 165 CCACGTGGAATT 176
XX
XX Db 5 CCACGTGGAATT 16
XX
XX RESULT 139
XX ABV85811
XX ID ABV85811 standard; DNA; 17 BP.
XX
XX AC ABV85811;
XX
XX 11-DEC-2002 (first entry)
XX
XX Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:804.
XX
XX Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
XX pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX ss.
XX Homo sapiens.
XX

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OS Synthetic.
XX
XX EP1243660-A2.
XX
XX 25-SEP-2002.
XX
XX 25-JAN-2002; 2002EP-00001161.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX and treat disorders associated with reduced or over expression of the
XX encoded protein.
XX
XX Example 2; SEQ ID NO 804; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
XX human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
XX chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX present invention can be used in therapy, particularly to prevent or
XX treat a disorder associated with decreased expression or activity of pp-
XX GaNTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
XX ABP53504 are given in the exemplification of the present invention. N.B.
XX The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied by the
XX European Patent Office
XX
XX Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 165 CCACGTGGAATT 176
XX
XX Db 6 CCACGTGGAATT 17
XX
XX RESULT 140
XX ABV85814
XX ID ABV85814 standard; DNA; 17 BP.
XX
XX AC ABV85814;
XX
XX 11-DEC-2002 (first entry)
XX
XX Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:807.
XX
XX Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
XX pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX ss.
XX Homo sapiens.
XX Synthetic.
XX EP1243660-A2.
XX

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XX 25-SEP-2002.
PD
XX
XX 25-JAN-2002; 2002EP-00001161.
PF
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
PT and treat disorders associated with reduced or over expression of the
PT encoded protein.
XX
XX Example 2; SEQ ID NO 807; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
CC human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
CC GANTase 10, EC 2.4.1.41) protein. Human pp-GANTase 10 is located to
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC present invention can be used in therapy, particularly to prevent or
CC treat a disorder associated with decreased expression or activity of pp-
CC GANTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
CC ABP53504 are given in the exemplification of the present invention. N.B.
CC The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office
XX
XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 CCACGTGGAATT 176
Db 3 CCACGTGGAATT 14
RESULT 141
ABV85815
ID ABV85815 standard; DNA; 17 BP.
XX
XX ABV85815;
AC
XX
XX 11-DEC-2002 (first entry)
DT
XX
XX Human pp-GANTase 10 scanning 17-mer SEQ ID NO:808.
DE
XX Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
KW pp-GANTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
KW ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX EP1243660-A2.
XX
XX EP1243660-A2.
XX
XX 25-SEP-2002.
XX
XX

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PF 25-JAN-2002; 2002EP-00001161.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
PT and treat disorders associated with reduced or over expression of the
PT encoded protein.
XX
XX Example 2; SEQ ID NO 808; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
CC human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
CC GANTase 10, EC 2.4.1.41) protein. Human pp-GANTase 10 is located to
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC present invention can be used in therapy, particularly to prevent or
CC treat a disorder associated with decreased expression or activity of pp-
CC GANTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
CC ABP53504 are given in the exemplification of the present invention. N.B.
CC The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office
XX
XX Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 165 CCACGTGGAATT 176
Db 2 CCACGTGGAATT 13
RESULT 142
ABV85816
ID ABV85816 standard; DNA; 17 BP.
XX
XX ABV85816;
AC
XX
XX 11-DEC-2002 (first entry)
DT
XX
XX Human pp-GANTase 10 scanning 17-mer SEQ ID NO:809.
DE
XX Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
KW pp-GANTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
KW ss.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX EP1243660-A2.
XX
XX EP1243660-A2.
XX
XX 25-SEP-2002.
XX
XX 25-JAN-2002; 2002EP-00001161.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX

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PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 30-AUG-2001; 2001US-0315984P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Zhang J, Gu Y, Nguyen C;  
XX WPI; 2002-724954/79.  
XX  
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-  
PT cetylglucosaminyltransferase 10 protein is useful to diagnose, prevent  
PT and treat disorders associated with reduced or over expression of the  
PT encoded protein.  
XX  
XX Example 2; SEQ ID NO 809; 59pp; English.  
XX  
XX The present invention describes an isolated nucleic acid (I) encoding a  
CC human UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10 (pp-  
CC GalNAc 10, EC 2.4.1.41) protein. Human pp-GalNAc 10 is located to  
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the  
CC present invention can be used in therapy, particularly to prevent or  
CC treat a disorder associated with decreased expression or activity of pp-  
CC GalNAc. The sequences given in ABV85011 to ABV86689 and ABP3502 to  
CC ABP3504 are given in the exemplification of the present invention. N.B.  
CC The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied by the  
CC European Patent Office  
XX  
XX Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 165 CCACGTGGAATT 176  
DB 1 CCACGTGGAATT 12  
RESULT 143  
ABV85813  
ID ABV85813 standard; DNA; 17 BP.  
XX  
XX ABV85813;  
AC  
XX  
XX 11-DEC-2002 (first entry)  
DT  
XX  
XX Human pp-GalNAc 10 scanning 17-mer SEQ ID NO:806.  
DE  
XX  
XX Human: UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10;  
KW pp-GalNAc 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;  
KW ss.  
XX  
XX Homo sapiens.  
XX OS  
XX Synthetic.  
XX  
XX PN EPI243660-A2.  
PN  
XX  
XX 25-SEP-2002.  
PD  
XX  
XX 25-JAN-2002; 2002EP-00001161.  
PF  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 23-MAY-2001; 2001US-00864761.  
PR 30-AUG-2001; 2001US-0315984P.  
XX  
XX (AEOM-) AEOMICA INC.  
XX  
XX Zhang J, Gu Y, Nguyen C;  
XX WPI; 2002-724954/79.  
XX  
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-  
PT cetylglucosaminyltransferase 10 protein is useful to diagnose, prevent  
PT and treat disorders associated with reduced or over expression of the  
PT encoded protein.  
XX  
XX Example 2; SEQ ID NO 806; 59pp; English.  
XX  
XX The present invention describes an isolated nucleic acid (I) encoding a  
CC human UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10 (pp-  
CC GalNAc 10, EC 2.4.1.41) protein. Human pp-GalNAc 10 is located to  
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the  
CC present invention can be used in therapy, particularly to prevent or  
CC treat a disorder associated with decreased expression or activity of pp-  
CC GalNAc. The sequences given in ABV85011 to ABV86689 and ABP3502 to  
CC ABP3504 are given in the exemplification of the present invention. N.B.  
CC The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied by the  
CC European Patent Office  
XX  
XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;  
SQ  
Query Match 2.0%; Score 12; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 165 CCACGTGGAATT 176  
DB 4 CCACGTGGAATT 15  
RESULT 144  
ABV79548/C  
ID ABV79548 standard; DNA; 17 BP.  
XX  
XX ABV79548;  
AC  
XX  
XX 03-JAN-2003 (first entry)  
DT  
XX  
XX Human HTPL scanning oligonucleotide SEQ ID 794.  
DE  
XX  
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;  
KW human testis expressed Patched like protein; testis; adrenal; liver;  
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;  
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.  
XX  
XX Homo sapiens.  
XX OS  
XX EPI229046-A2.  
XX PN  
XX 07-AUG-2002.  
PD  
XX  
XX 28-JAN-2002; 2002EP-00001167.  
PF  
XX  
XX 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 23-MAY-2001; 2001US-00864761.

```

PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPPL.
XX
XX Example 2; Page 167; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPPL is
CC important in regulating male germ cell development, and the HTPPL gene was
CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 386 TGCACCGCGCGC 397
DB 17 TGCACCGCGCGC 6
RESULT 145
ABV79554/C
ID ABV79554 standard; DNA; 17 BP.
XX
XX ABV79554;
XX
XX 03-JAN-2003 (first entry)
XX
XX Human HTPPL scanning oligonucleotide SEQ ID 800.
XX
XX Human; Gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EPI229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EB-00001167.
XX
XX 30-JAN-2001; 2001MO-US000663.
XX
XX 30-JAN-2001; 2001MO-US000664.
XX
XX 30-JAN-2001; 2001MO-US000665.
XX
XX 30-JAN-2001; 2001MO-US000667.
XX
XX 30-JAN-2001; 2001MO-US000668.

```

```

PR 30-JAN-2001; 2001MO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPPL.
XX
XX Example 2; Page 168; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPPL is
CC important in regulating male germ cell development, and the HTPPL gene was
CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 CTGCACCGCGCC 396
DB 12 CTGCACCGCGCC 1
RESULT 146
ACC53318
ID ACC53318 standard; DNA; 17 BP.
XX
XX ACC53318;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #2085.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX
XX FR2826373-A1.
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX

```

PI Tuijnder M, Telerman A, Amson R;  
 XX WPI; 2003-250498/25.  
 XX  
 PT New nucleic acid sequences associated with tumor suppression, regression,  
 PT apoptosis or virus resistance are useful to diagnose and treat viral  
 PT disease, development of tumor cells and cell degeneration.  
 XX  
 PS Claim 1; Page 521; 798bp; French.  
 CC This sequence represents an isolated nucleic acid sequence associated  
 CC with tumor suppression or regression, apoptosis or virus resistance. The  
 CC invention relates to these sequences or sequences having at least 80%  
 CC identity to them, and polypeptides encoded by the sequences or  
 CC polypeptides having 80% identity to the polypeptide sequences. The  
 CC invention is used to diagnose or treat viral disease or disease  
 CC characterized by development of tumour cells or cellular degeneration  
 XX  
 SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 355 CGCAGGCTGAG 366  
 Db 4 CGCAGGCTGAG 15  
 RESULT 147  
 ABT37905  
 ID ABT37905 standard; DNA; 17 BP.  
 XX ABT37905;  
 AC  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID No 3542.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; protein chip; gene therapy; tumour suppression;  
 KM human fukutin; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025175-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002MO-IB004208.  
 XX  
 PR 17-SEP-2001; 2001FR-00011978.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 448; 720pp; French.  
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, or the complement  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,

CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterized by development of tumours or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention  
 XX  
 SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 355 CGCAGGCTGAG 366  
 Db 4 CGCAGGCTGAG 15  
 RESULT 148  
 ABT36423/c  
 ID ABT36423 standard; DNA; 17 BP.  
 XX ABT36423;  
 AC  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID No 2060.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; protein chip; gene therapy; tumour suppression;  
 KM human fukutin; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025175-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002MO-IB004208.  
 XX  
 PR 17-SEP-2001; 2001FR-00011978.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 273; 720pp; French.  
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, or the complement  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for

CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the  
 CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterized by development of tumors or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention

XX  
 SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 AGCTGAGGATC 324  
 Db 12 AGCTGAGGATC 1

RESULT 149  
 ADBT34697  
 ID ABT34697 standard; DNA; 17 BP.  
 AC ABT34697;  
 XX  
 DT 12-JUN-2003 (first entry)  
 XX  
 DE Tumour suppression related human fukutin oligo SEQ ID NO 334.  
 XX  
 KM Cytostatic; vinicide; neuroprotective; nootropic; neuroleptic; gene chip;  
 KM antiense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; protein chip; gene therapy; tumour suppression;  
 KM human fukutin; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003025175-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB04208.  
 XX  
 PR 17-SEP-2001; 2001FR-00011978.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijinder M;  
 XX  
 DR WPI; 2003-313353/30.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 73; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,  
 CC given in the specification, a sequence containing at least 15 consecutive  
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal  
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that  
 CC hybridizes to them under highly stringent conditions, or the complement  
 CC of any of them, or the corresponding RNA. The novel isolated nucleic  
 CC acids of the invention are useful as probes and primers for detecting,  
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one  
 CC component of a gene chip, in vitro as (anti)sense reagents, and for  
 CC production of recombinant polypeptides. Any of the nucleic acids,  
 CC polypeptides, vectors containing the nucleic acids, cells containing the

CC vector or antibodies directed against the polypeptides are useful for  
 CC preparation of pharmaceuticals for prevention and/or treatment of viral  
 CC diseases that are characterized by development of tumors or cell  
 CC degeneration, specifically cancer but also Alzheimer's disease and  
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in  
 CC patient samples is useful for diagnosis and/or prognosis of these  
 CC diseases. The polypeptides can also be used to generate antibodies, and  
 CC both the polypeptide and antibodies are useful as components of protein  
 CC chips. The nucleic acid sequences of the invention can be used in gene  
 CC therapy. This polynucleotide sequence represents a tumour suppression  
 CC related human fukutin oligonucleotide of the invention

XX  
 SQ Sequence 17 BP; 8 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ACCATGAAGAA 472  
 Db 5 ACCATGAAGAA 16

RESULT 150  
 ADB03447/C  
 ID ADB03447 standard; DNA; 17 BP.  
 XX  
 AC ADB03447;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human MD27 scanning oligonucleotide SEQ ID 4433.  
 XX  
 KM Cytostatic; immunostimulant; gene therapy; vaccine; human;  
 KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 6p21.3-22.1;  
 KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
 KM developmental disorder; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 PT manufacturing a medicament for treating or preventing a disorder  
 PT associated with decreased or increased expression or activity of MD23,  
 PT MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 4433; 103pp; English.

XX The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q42.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.  
XX

SO Sequence 17 BP; 1 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGCGC 376

DB 12 AGCCCGAGGCGC 1

RESULT 151

ADA99804

ADA99804 standard; DNA; 17 BP.

AC ADA99804;

DT 20-NOV-2003 (first entry)

DE Human MD23 scanning oligonucleotide SEQ ID 793.

OS Cytostatic; immunostimulant; gene therapy; vaccine; human;

KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KM developmental disorder; ss.

OS Homo sapiens.

XX EPI281758-A2.

PN 05-FEB-2003.

PD 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

PS Example 8; SEQ ID NO 793; 103bp; English.

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 3 C; 5 G; 7 T; 0 U; 0 Other;

SO Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGCA 445

DB 6 TTACTGCTGCA 17

RESULT 152

ADA99805

ADA99805 standard; DNA; 17 BP.

AC ADA99805;

DT 20-NOV-2003 (first entry)

DE Human MD23 scanning oligonucleotide SEQ ID 794.

OS Cytostatic; immunostimulant; gene therapy; vaccine; human;

KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KM developmental disorder; ss.

OS Homo sapiens.

XX EPI281758-A2.

PN 05-FEB-2003.

PD 30-JUL-2002; 2002EP-00016874.

PR 02-AUG-2001; 2001US-00922181.

PA (AEOM-) AEOMICA INC.

PI Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

PS Example 8; SEQ ID NO 794; 103bp; English.

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

SO Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGCA 445

DB 5 TTACTGCTGCA 16

RESULT 153

```

ADA99323/c
ID ADA99323 standard; DNA; 17 BP.
XX
AC ADA99323;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 312.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WP1; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 312; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 247 TCCTGAGAGCCCC 258
DB 17 TCCTGAGAGCCCC 6

```

```

XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WP1; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 795; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 434 TTTACTGCTGGA 445
DB 4 TTTACTGCTGGA 15

```

```

RESULT 154
ADA99806
ID ADA99806 standard; DNA; 17 BP.
XX
AC ADA99806;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 795.

```

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RESULT 155
ADB03443/c
ID ADB03443 standard; DNA; 17 BP.
XX
AC ADB03443;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 4429.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX

```

```

XX  EPI281758-A2.
XX
PD  05-FEB-2003.
XX
PF  30-JUL-2002; 2002EP-00016874.
XX
PR  02-AUG-2001; 2001US-00922181.
XX
PA  (AEOM-) AEOMICA INC.
XX
PI  Shannon M, Gu Y, Nguyen C;
XX
DR  WPI; 2003-423107/40.
XX
PT  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder
PT  associated with decreased or increased expression or activity of MD23,
PT  MD24, MD27 or MD212, e.g. cancer.
XX
PS  Example 8; SEQ ID NO 4429; 103bp; English.
XX
CC  The present invention relates to novel human zinc finger-containing
CC  proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC  encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC  MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC  15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC  or in manufacturing a medicament for treating or preventing a disorder
CC  associated with decreased or increased expression or activity of MD23,
CC  MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC  acids and proteins are also useful for diagnosing or monitoring a disease
CC  caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC  acids can also be used as probes to detect and characterize gross
CC  alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC  useful in constructing microarrays for measuring gene expression. The
CC  proteins are useful as therapeutic agents for gene therapy or as
CC  vaccines. The present sequence was used to illustrate the invention.
XX
SQ  Sequence 17 BP; 0 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  365 AGCCCGAGGGGC 376
    |||||
    16 AGCCCGAGGGGC 5
XX
Db
XX
RESULT 156
ADB03445/c
ID  ADB03445 standard; DNA; 17 BP.
XX
AC  ADB03445;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 4431.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW  chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW  developmental disorder; ss.
XX
OS  Homo sapiens.
XX
PN  EPI281758-A2.
XX
PD  05-FEB-2003.
XX
PF  30-JUL-2002; 2002EP-00016874.
XX
PR  02-AUG-2001; 2001US-00922181.
XX

```

```

PA  (AEOM-) AEOMICA INC.
XX
PI  Shannon M, Gu Y, Nguyen C;
XX
DR  WPI; 2003-423107/40.
XX
PT  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder
PT  associated with decreased or increased expression or activity of MD23,
PT  MD24, MD27 or MD212, e.g. cancer.
XX
PS  Example 8; SEQ ID NO 4431; 103bp; English.
XX
CC  The present invention relates to novel human zinc finger-containing
CC  proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC  encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC  MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC  15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC  or in manufacturing a medicament for treating or preventing a disorder
CC  associated with decreased or increased expression or activity of MD23,
CC  MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC  acids and proteins are also useful for diagnosing or monitoring a disease
CC  caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC  acids can also be used as probes to detect and characterize gross
CC  alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC  useful in constructing microarrays for measuring gene expression. The
CC  proteins are useful as therapeutic agents for gene therapy or as
CC  vaccines. The present sequence was used to illustrate the invention.
XX
SQ  Sequence 17 BP; 0 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY  365 AGCCCGAGGGGC 376
    |||||
    14 AGCCCGAGGGGC 3
XX
Db
XX
RESULT 157
ADB03446/c
ID  ADB03446 standard; DNA; 17 BP.
XX
AC  ADB03446;
XX
DT  20-NOV-2003 (first entry)
XX
DE  Human MD27 scanning oligonucleotide SEQ ID 4432.
XX
KW  Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW  zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW  chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW  developmental disorder; ss.
XX
OS  Homo sapiens.
XX
PN  EPI281758-A2.
XX
PD  05-FEB-2003.
XX
PF  30-JUL-2002; 2002EP-00016874.
XX
PR  02-AUG-2001; 2001US-00922181.
XX
PA  (AEOM-) AEOMICA INC.
XX
PI  Shannon M, Gu Y, Nguyen C;
XX
DR  WPI; 2003-423107/40.
XX
PT  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder

```

PT associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27 or MD212, e.g. cancer.  
 XX Example 8; SEQ ID NO 443; 103bp; English.  
 PS  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 CC  
 XX Sequence 17 BP; 1 A; 7 C; 6 G; 3 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 365 AGCCCGAGGGGC 376  
 Db 13 AGCCCGAGGGGC 2  
 RESULT 158  
 ADA99807  
 ID ADA99807 standard; DNA; 17 BP.  
 AC ADA99807;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE Human MD23 scanning oligonucleotide SEQ ID 796.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 CC manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 796; 103bp; English.  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross  
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are  
 CC useful in constructing microarrays for measuring gene expression. The  
 CC proteins are useful as therapeutic agents for gene therapy or as  
 CC vaccines. The present sequence was used to illustrate the invention.  
 CC  
 XX Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 434 TTACTCTCTCGA 445  
 Db 3 TTACTCTCTCGA 14  
 RESULT 159  
 ADA99809  
 ID ADA99809 standard; DNA; 17 BP.  
 AC ADA99809;  
 XX  
 DT 20-NOV-2003 (first entry)  
 DE Human MD23 scanning oligonucleotide SEQ ID 798.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1281758-A2.  
 XX  
 PD 05-FEB-2003.  
 XX  
 PF 30-JUL-2002; 2002EP-00016874.  
 XX  
 PR 02-AUG-2001; 2001US-00922181.  
 XX  
 PA (AEOM-) AEOMICA INC.  
 XX  
 PI Shannon M, Gu Y, Nguyen C;  
 XX  
 DR WPI; 2003-423107/40.  
 XX  
 PT New zinc finger-containing proteins and nucleic acids, useful in  
 CC manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27 or MD212, e.g. cancer.  
 XX  
 PS Example 8; SEQ ID NO 798; 103bp; English.  
 CC The present invention relates to novel human zinc finger-containing  
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is  
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,  
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome  
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,  
 CC or in manufacturing a medicament for treating or preventing a disorder  
 CC associated with decreased or increased expression or activity of MD23,  
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic  
 CC acids and proteins are also useful for diagnosing or monitoring a disease  
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic  
 CC acids can also be used as probes to detect and characterize gross

CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

SEQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 TTTACTGCTGGA 445  
1 TTTACTGCTGGA 12

RESULT 160  
ADB03442/C  
ID ADB03442 standard; DNA; 17 BP.  
XX  
AC ADB03442;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human MDZ7 scanning oligonucleotide SEQ ID 4428.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.

OS Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 4428; 103bp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 0 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 365 AGCCCGAGGGGC 376  
Db 17 AGCCCGAGGGGC 6

RESULT 161  
ADA99329/C  
ID ADA99329 standard; DNA; 17 BP.

XX ADA99329;  
XX  
DT 20-NOV-2003 (first entry)  
XX

DE Human MDZ3 scanning oligonucleotide SEQ ID 318.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;  
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;  
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;  
XX developmental disorder; ss.

OS Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in  
PT manufacturing a medicament for treating or preventing a disorder  
PT associated with decreased or increased expression or activity of MDZ3,  
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.

XX Example 8; SEQ ID NO 318; 103bp; English.

XX The present invention relates to novel human zinc finger-containing  
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is  
CC encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,  
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome  
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,  
CC or in manufacturing a medicament for treating or preventing a disorder  
CC associated with decreased or increased expression or activity of MDZ3,  
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic  
CC acids and proteins are also useful for diagnosing or monitoring a disease  
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic  
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are  
CC useful in constructing microarrays for measuring gene expression. The  
CC proteins are useful as therapeutic agents for gene therapy or as  
CC vaccines. The present sequence was used to illustrate the invention.

XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGAGGCC 257  
Db 12 CTCCTGAGGCC 1

```

RESULT 162
ADB03444/c
ID ADB03444 standard; DNA; 17 BP.
XX
XX ADB03444;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 4430.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 4430; 103pp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ

```

```

Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      365 AGCCCGAGGGGC 376
      |||||
      15 AGCCCGAGGGGC 4

```

```

RESULT 163
ADA9808
ID ADA9808 standard; DNA; 17 BP.
XX
XX ADA9808;
AC
XX
XX 20-NOV-2003 (first entry)
DT
XX

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```

DE Human MD23 scanning oligonucleotide SEQ ID 797.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (AEOM-) AEOMICA INC.
PA
XX
XX Shannon M, Gu Y, Nguyen C;
PI
XX
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 797; 103pp; English.
PS
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
SQ

```

```

Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      434 TTTACTGCTGCA 445
      |||||
      2 TTTACTGCTGCA 13

```

```

RESULT 164
ABZ61994/c
ID ABZ61994 standard; RNA; 17 BP.
XX
XX ABZ61994;
AC
XX
XX 21-MAR-2003 (first entry)
DT
XX
XX Human H-Ras DNAzyme target #785.
DE
XX
XX Human, ribozyme; short interfering RNA; siRNA; H-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
OS
XX

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PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 126; 185pp; English.
XX
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
XX CC ribozymes of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 CCCCAACTCAG 314
DB 15 CCCCAACTCAG 4

RESULT 165
ABZ61385
ID ABZ61385 standard; RNA; 17 BP.
XX
XX AC ABZ61385;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human H-Ras DNAzyme target #176.
XX
XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KM anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.

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XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 114; 185pp; English.
XX
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
XX CC ribozymes of the invention
XX
SQ Sequence 17 BP; 0 A; 4 C; 12 G; 0 T; 1 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGGCTGCGGCGG 384
DB 1 GGGCTGCGGCGG 12

RESULT 166
ABZ61383
ID ABZ61383 standard; RNA; 17 BP.
XX
XX AC ABZ61383;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human H-Ras DNAzyme target #174.
XX
XX KM Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KM anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 114; 185pp; English.

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CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention

XX  
SQ Sequence 17 BP; 0 A; 5 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
Best Local Similarity 91.7%; Pred. No. 1.2e+05;  
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 372 GGGGCTGCGGCG 383  
Db 6 GGGGCTGCGGCG 17

RESULT 167  
ABZ61791/C  
ID ABZ61791 standard; RNA; 17 BP.  
XX  
AC ABZ61791;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human H-Ras DNAzyme target #582.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
KM anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US016840.  
XX  
PR 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 10-SEP-2001; 2001US-0318471P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
DR WPI; 2003-140484/13.  
XX  
PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
PS Claim 58; Page 122; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human

CC ribozymes of the invention

XX  
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 CTGTGCCGACCA 278  
Db 12 CTGTGCCGACCA 1

RESULT 168  
ABZ61790/C  
ID ABZ61790 standard; RNA; 17 BP.  
XX  
AC ABZ61790;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human H-Ras DNAzyme target #581.  
XX  
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;  
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;  
KM anti-rheumatic; cancer; AIDS; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200297114-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002WO-US016840.  
XX  
PR 29-MAY-2001; 2001US-0294140P.  
PR 06-JUN-2001; 2001US-0296249P.  
PR 10-SEP-2001; 2001US-0318471P.  
XX  
PA (RIBO-) RIBOZYME PHARM INC.  
XX  
PI Mcswiggen J;  
XX  
DR WPI; 2003-140484/13.  
XX  
PT Novel short interfering RNA and enzymatic nucleic acid useful for  
PT treating cancer, modulates the expression of a nucleic acid encoding  
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.  
XX  
PS Claim 58; Page 122; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention

XX  
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 CTGTGCCGACCA 278  
Db 14 CTGTGCCGACCA 3

RESULT 169  
 ACC64654  
 ID ACC64654 standard; DNA; 17 BP.  
 XX  
 AC ACC64654;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1901.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 XX schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-333167/31.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 253; 738pp; French.  
 XX  
 CC The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68906), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX  
 SO Sequence 17 BP; 5 A; 5 C; 3 G; 4 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 75 TGAAGACTTACT 86  
 Db 5 TGAAGACTTACT 16  
 XX  
 RESULT 170  
 ACC65317  
 ID ACC65317 standard; DNA; 17 BP.  
 XX  
 AC ACC65317;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2564.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;  
 XX

KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; ss.  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX  
 PI Telerman A, Amson R, Tuijnder M;  
 XX WPI; 2003-333167/31.  
 XX  
 DR WPI; 2003-333167/31.  
 XX  
 PT New isolated nucleic acid, useful for treating viral diseases associated  
 PT with tumors and cell degeneration, also related polypeptides, antibodies  
 PT and transfected cells.  
 XX  
 PS Disclosure; Page 330; 738pp; French.  
 XX  
 CC The present invention relates to murine oligonucleotides (ACC62754-  
 CC ACC68906), which are associated with tumour suppression, tumour  
 CC reversion, apoptosis and virus resistance. The oligonucleotides are  
 CC useful as (1) as probes and primers for detecting, identifying,  
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a  
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a  
 CC recombinant polypeptides. The oligonucleotides are useful for preparation  
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that  
 CC are characterised by development of tumours or cell degeneration,  
 CC specifically cancer but also Alzheimer's disease and schizophrenia  
 XX  
 SO Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 7; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 CTGAGCTTGGT 141  
 Db 6 CTGAGCTTGGT 17  
 XX  
 RESULT 171  
 ACC64816/C  
 ID ACC64816 standard; DNA; 17 BP.  
 XX  
 AC ACC64816;  
 XX  
 DT 01-JUL-2003 (first entry)  
 XX  
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2063.  
 XX  
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;  
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;  
 KM schizophrenia; ss.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003025176-A2.  
 XX  
 PD 27-MAR-2003.  
 XX  
 PF 17-SEP-2002; 2002WO-IB004210.  
 XX  
 PR 17-SEP-2001; 2001FR-00011979.  
 XX  
 PA (MOLE-) MOLECULAR ENGINES LAB.  
 XX

Pt Telerman A., Amson R., Tuijinder M;  
Dr WPI; 2003-333167/31.  
XX  
Pt New isolated nucleic acid, useful for treating viral diseases associated  
with tumors and cell degeneration, also related polypeptides, antibodies  
Pr and transfected cells.  
Xx  
Ps Disclosure; Page 272; 738pp; French.

Cc The present invention relates to murine oligonucleotides (ACC62754-  
Cc ACC698806), which are associated with tumour suppression, tumour  
Cc reversion, apoptosis and virus resistance. The oligonucleotides are  
Cc useful as (1) as probes and primers for detecting, identifying,  
Cc quantifying and/or amplifying nucleic acid, e.g. as one component of a  
Cc gene chip; in vitro as (anti)sense reagents; and (2) for production of  
Cc recombinant polypeptides. The oligonucleotides are useful for preparation  
Cc of pharmaceuticals for prevention and/or treatment of viral diseases that  
Cc are characterised by development of tumours or cell degeneration,  
Cc specifically cancer but also Alzheimer's disease and schizophrenia

Sq Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Oy Query March 2 0%; Score 12; DB 7; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Xy 457 GAAGACCATGAA 468  
||| ||| |  
Db 17 GAAGACCATGAA 6

Rz RESULT 172  
ADBA0734/C  
ID ADBA0734 standard; DNA; 17 BP.  
Xx  
Ac ADBA0734;  
Xx  
Dt 18-DEC-2003 (revised)  
Df 04-DEC-2003 (first entry)

Dd Tumour suppression/reversion associated nucleotide #1057.  
Xe cyostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;  
Xv primer; probe; tumour suppression; tumour reversion; apoptosis;  
Xw virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
diagnosis.  
Xx Homo sapiens.  
Cs  
Pn WO2003040369-A2.  
Pd 15-MAY-2003.  
Pf 17-SEP-2002; 2002WO-IBO04219.  
Pr 17-SEP-2001; 2001FR-00011981.  
Pa (MOLE-) MOLECULAR ENGINES LAB.  
Px Teleman A.; Amson R., Tuijinder M;  
Pl WPI; 2003-441574/41.  
Dr  
Xx New nucleic acid encoding human prostate membrane-specific antigen,  
Pt useful e.g. for treatment of tumors and viral infection, also related  
FT polypeptide and antibodies.  
Xx  
Ps Disclosure; Page 155; 771pp; French.

Cc The invention relates to the isolation of 6327 nucleotide sequences,  
Cc fragments of at least 15 consecutive nucleotides of these nucleotides, a

CC	sequence having at least 80% identity, after optimal alignment, with the
CC	nucleotides, a sequence that hybridizes under stringent conditions with
CC	the nucleotides, or the complement, or corresponding RNA, of the
CC	nucleotides. The nucleotides are used as probes or primers for detecting,
CC	identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC	sense and antisense sequences, of nucleotides involved in tumour
CC	suppression or reversion, apoptosis and/or viral resistance, to produce
CC	recombinant polypeptides, and to prepare transgenic animals, as
CC	experimental models. The nucleotides (also vectors containing them and
CC	cells containing the vectors), the encoded polypeptides and antibodies
CC	(Ab) against the polypeptide are useful for prevention and/or treatment
CC	of viral infections or diseases characterised by development of tumours
CC	or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC	Analysis of the expression of the nucleotides can be used for diagnosis
CC	and/or prognosis of these diseases. The nucleotides and polypeptides can
CC	also be used to screen for their specific interactive molecules,
CC	potentially useful for treating diseases associated with abnormal
CC	expression of the nucleotides.
XX	
SO	Sequence 17 BP, 5 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
	Query Match 2.0%; Score 12; DB 9; Length 17;
	Best Local Similarity 100.0%; Pred. No. 1,2e+05;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	500 AAAATTCAGTTC 511
	17 AAAATTCAGTTC 6
Db	
RESULT 173	
ADB43195	
ID	ADB43195 standard; DNA; 17 BP.
XX	
AC	ADB43195;
XX	
DT	18-DEC-2003 (revised)
DT	04-DEC-2003 (first entry)
XX	
XX	Tumour suppression/reversion associated nucleotide #3518.
DE	
XX	
KW	cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW	primer; probe; tumour suppression; tumour reversion; apoptosis;
KW	virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX	diagnosis.
XX	
OS	Homo sapiens.
XX	
FN	WO2003040369-A2.
XX	
PD	15-MAY-2003.
XX	
PE	17-SEP-2002; 2002WO-1B004219.
XX	
PR	17-SEP-2001; 2001FR-00011981.
XX	
PA	(MOLE-) MOLECULAR ENGINES LAB.
XX	
PI	Telerman A, Amson R, Tuijnder M;
XX	
DR	WPI; 2003-441574/41.
XX	
PT	New nucleic acid encoding human prostate membrane-specific antigen,
XX	useful e.g. for treatment of tumors and viral infection, also related
PT	polypeptide and antibodies.
XX	
PS	Disclosure; Page 443; 771pp; French.
XX	
XX	The invention relates to the isolation of 6327 nucleotide sequences,
CC	fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC	sequence having at least 80% identity, after optimal alignment, with the
CC	nucleotides; a sequence that hybridizes under stringent conditions with
CC	the nucleotides, or the complement or corresponding RNA, of the

CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, or nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce  
 CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.

SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGAG 366  
 Db 4 CGCAGGCTGAG 15

RESULT 174  
 ADB45286  
 ID ADB45286 standard; DNA; 17 BP.  
 XX  
 AC ADB45286;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DT  
 XX  
 DE Tumour suppression/reversion associated nucleotide #5609.  
 DE  
 XX  
 KW cytosolic; antiviral; neuroprotective; nocitropic; neuroleptic; ss;  
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;  
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;  
 KW diagnosis.  
 XX  
 OS Homo sapiens.  
 OS  
 PN MO2003040369-A2.  
 PN  
 PD 15-MAY-2003.  
 PD  
 XX  
 PF 17-SEP-2002; 2002WO-1B004219.  
 PF  
 XX  
 PR 17-SEP-2001; 2001FR-00011981.  
 PR  
 XX  
 PA (MOLE-) MOLECULAR ENGINEES LAB.  
 PA  
 XX  
 PI Tejerman A, Amson R, Tuijnder M;  
 PI  
 XX  
 DR WPI; 2003-441574/41.  
 DR  
 XX  
 FT New nucleic acid encoding human prostate membrane-specific antigen,  
 FT useful e.g. for treatment of tumors and viral infection, also related  
 PT polypeptide and antibodies.  
 PT  
 XX  
 PS Disclosure; Page 687; 771pp; French.  
 PS  
 XX  
 CC The invention relates to the isolation of 6327 nucleotide sequences,  
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a  
 CC sequence having at least 80% identity, after optimal alignment, with the  
 CC nucleotides, a sequence that hybridizes under stringent conditions with  
 CC the nucleotides, or the complement, or corresponding RNA, of the  
 CC nucleotides. The nucleotides are used as probes or primers for detecting,  
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro  
 CC sense and antisense sequences, of nucleotides involved in tumour  
 CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as  
 CC experimental models. The nucleotides (also vectors containing them and  
 CC cells containing the vectors), the encoded polypeptides and antibodies  
 CC (Ab) against the polypeptide are useful for prevention and/or treatment  
 CC of viral infections or diseases characterized by development of tumours  
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).  
 CC Analysis of the expression of the nucleotides can be used for diagnosis  
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can  
 CC also be used to screen for their specific interactive molecules,  
 CC potentially useful for treating diseases associated with abnormal  
 CC expression of the nucleotides.

SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 9; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGAG 366  
 Db 4 CGCAGGCTGAG 15

RESULT 175  
 AAQ06031/c  
 ID AAQ06031 standard; DNA; 18 BP.  
 XX  
 AC AAQ06031;  
 AC  
 XX  
 DT 17-DEC-2001 (revised)  
 DT  
 XX  
 DT 08-MAR-1992 (first entry)  
 DT  
 XX  
 DE Sequence of VP1 (-) sense probe for nucleotides 2283-2301 of VP1 amino  
 DE terminal genome region.  
 DE  
 XX  
 KW Detection; hepatitis A virus; viral protein 1; polymerase chain reaction;  
 KW ss.  
 KW  
 XX  
 OS Hepatitis A virus.  
 OS  
 PN USN7469143-N.  
 PN  
 PD 04-SEP-1990.  
 PD  
 XX  
 PF 24-JAN-1990; 90US-00469143.  
 PF  
 XX  
 PR 24-JAN-1990; 90US-00469143.  
 PR  
 XX  
 PA (USSH ) NAT INST OF HEALTH.  
 PA (USDC ) US SEC OF COMMERCE.  
 PA  
 XX  
 DR WPI; 1990-304798/40.  
 DR  
 XX  
 PT Detection of hepatitis A virus in samples - by extracting RNA,  
 PT synthesising cDNA, amplifying the cDNA by PCR and detecting amplified  
 PT prod.  
 PT  
 XX  
 PS Disclosure; Page 6; 28pp; English.  
 PS  
 XX  
 CC The labelled probes whose SQs are given in AAQ06030-2 are used for  
 CC detecting amplified VP1 amino terminal genome region HAV cDNA. The method  
 CC of the invention provides a rapid, sensitive and specific test for  
 CC detecting the presence of HAV in infected or contaminated samples of  
 CC e.g., stools, serum, water or foodstuffs such as shellfish. (Note:  
 CC Revised entry submitted to correct the patent number format of US  
 CC Government-owned NTIS applications to prevent clashes with ongoing US  
 CC granted patent numbers. For further information please visit the Derwent  
 CC web site at [www.derwent.com/dwpi/updates/ntis\\_us.html](http://www.derwent.com/dwpi/updates/ntis_us.html).)  
 CC  
 XX  
 SQ Sequence 18 BP; 4 A; 2 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 AACCATGAAGA 471  
 |||||  
 DB 16 AACCATGAAGA 5

RESULT 176  
 AAQ26186/c  
 ID AAQ26186 standard; DNA; 18 BP.

XX AAQ26186;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 04-JAN-1993 (first entry)  
 XX  
 DE HLA-DR beta sub-type tailed probe DRB82 hybridising region.

XX Tissue typing; identity determination; disease susceptible; ss.

XX Synthetic.

XX WO9210589-A1.

XX 25-JUN-1992.

XX 06-DEC-1991; 91WO-US009294.

XX 06-DEC-1990; 90US-00623098.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;

XX Apple RJ;

XX WPI; 1992-234644/28.

PT Method for determining HLA-DR beta sub-type in DNA sample - comprises  
 PT amplification and hybridisation with probes and primers, useful in tissue  
 PT typing.

PS Example; Page 39; 90pp; English.

XX The sequence is that of the hybridising region of tailed probe DRB82 for  
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid  
 CC sample. The method allows specific nucleic acid sequences of the second  
 CC exon of HLA-DR beta genes to be amplified then probed for identification  
 CC of polymorphic sequences. The amplified DNA is useful for typing  
 CC homozygous or heterozygous samples from a variety of sources and for  
 CC detecting allelic variants not distinguishable by serological methods.  
 CC The typing system can be used in a reverse dot blot format which is  
 CC simple and rapid to perform, produces detectable signals in minutes and  
 CC can be utilised in tissue typing, determination of individual identity  
 CC and identifying disease susceptible individuals. See also AAQ26092-  
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255  
 |||||  
 DB 17 ACCTCCTGGAGC 6

RESULT 177  
 AAQ26149  
 ID AAQ26149 standard; DNA; 18 BP.  
 XX  
 XX AAQ26149;  
 AC  
 XX

DT 25-MAR-2003 (revised)  
 DT 04-JAN-1993 (first entry)  
 XX

DE HLA-DR beta sub-type tailed probe DRB84 hybridising region.

XX Tissue typing; identity determination; disease susceptible; ss.

XX Synthetic.

XX WO9210589-A1.

XX 25-JUN-1992.

XX 06-DEC-1991; 91WO-US009294.

XX 06-DEC-1990; 90US-00623098.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;

XX Apple RJ;

XX WPI; 1992-234644/28.

PT Method for determining HLA-DR beta sub-type in DNA sample - comprises  
 PT amplification and hybridisation with probes and primers, useful in tissue  
 PT typing.

PS Example; Page 38; 90pp; English.

XX The sequence is that of the hybridising region of tailed probe DRB44 for  
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid  
 CC sample. The method allows specific nucleic acid sequences of the second  
 CC exon of HLA-DR beta genes to be amplified then probed for identification  
 CC of polymorphic sequences. The amplified DNA is useful for typing  
 CC homozygous or heterozygous samples from a variety of sources and for  
 CC detecting allelic variants not distinguishable by serological methods.  
 CC The typing system can be used in a reverse dot blot format which is  
 CC simple and rapid to perform, produces detectable signals in minutes and  
 CC can be utilised in tissue typing, determination of individual identity  
 CC and identifying disease susceptible individuals. See also AAQ26092-  
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 3 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255  
 |||||  
 DB 2 ACCTCCTGGAGC 13

RESULT 178

AAQ38340  
 ID AAQ38340 standard; DNA; 18 BP.

XX AAQ38340;

XX 25-MAR-2003 (revised)

DT 15-JUN-1993 (first entry)

XX EcoRI primer 3 for SRPA of corn DNA with multiple restriction enzymes.

XX Restriction fragment; PCR; RFLP; forensic typing; Zee mays; ss; labeled;

XX selective restriction fragment amplification.

XX Synthetic.

XX BP534858-A1.  
 XX 31-MAR-1993.  
 PD

```

XX 24-SEP-1992; 92BP-00402629.
XX 24-SEP-1991; 91BP-00402542.
XX (KEYG-) KEYGENE NV.
XX Zabeau M, Vos P;
XX WPI; 1993-102942/13.
XX
XX Selective controlled restriction fragment amplification of DNA - used for
XX gene analysis e.g. DNA fingerprinting, restriction fragment length
XX polymorphisms, etc.
XX
XX Example 4; Page 18; 43pp; English.
XX
XX The DNA from two corn inbred lines was restricted with TaqI and one of
XX AseI, PstI, EcoRI or Sse8387-I and tagged with the appropriate adaptors.
XX This DNA was used as template in PCR reactions using one of the labelled
XX TaqI primers, 1-4 and one of PstI primers 1-4, AseI- primers 1-4, EcoRI-
XX primers 1-4 or Sse8387-I primers 1-4, each primer confg. three selective
XX nucleotides at the 3' end. A total of 128 PCRs was performed and the
XX reaction prods. analysed. All primer combinations gave DNA fingerprints
XX of 50-100 bands per lane, except for the combination SseI/TaqI, which
XX gave only 10-15 bands per lane. The method can be used to identify
XX preselected DNA fragments which can be polymorphic, i.e. RFLPs. It is a
XX superior method for multiplex PCR. The method may also be used to detect
XX similarities between plant or animal varieties, species etc, or for
XX evaluating genetic distances and characterizing the plant. See also
XX AAQ38313-43 and AAQ38907-16. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 18 BP; 5 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 36 TTACCAATCAA 47
XX |||||
XX Db 6 TTACCAATCAA 17
XX
XX RESULT 179
XX AAQ34757 standard; DNA; 18 BP.
XX
XX AC AAQ34757;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-JUN-1993 (first entry)
XX
XX DE Activator oligonucleotide probe p53(A).
XX
XX KM Human; p53; anti-oncogene; assay; ss.
XX
XX OS Synthetic;
XX
XX PN WO9301313-A1.
XX
XX PD 21-JAN-1993.
XX
XX PF 06-JUL-1992; 92WO-GB001225.
XX
XX FR 05-JUL-1991; 91GB-00014525.
XX
XX PA (CYTO-) CYTOCELL LTD.
XX
XX PI Cardy DLM, Delnatte SYU;
XX
XX DR WPI; 1993-045514/05.
XX

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PT Homogeneous assay for nucleic acid sequences - obtd. by modulating enzyme
PT activity, by hybridisation of derived nucleic acid probes.
XX
XX Example 2; Page 27; 51pp; English.
XX
XX The activator oligonucleotide probe p53(A) may be used in an assay for
XX the detection of the human p53 anti-oncogene in human DNA. See also
XX AAQ34750-62. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 ATGAACCGAGG 27
XX |||||
XX Db 4 ATGAACCGAGG 15
XX
XX RESULT 180
XX AAQ34759/c
XX ID AAQ34759 standard; DNA; 18 BP.
XX
XX AC AAQ34759;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-JUN-1993 (first entry)
XX
XX DE Blocker oligonucleotide p53(B).
XX
XX KM Human; p53; anti-oncogene; assay; ss.
XX
XX OS Synthetic.
XX
XX PN WO9301313-A1.
XX
XX PD 21-JAN-1993.
XX
XX PF 06-JUL-1992; 92WO-GB001225.
XX
XX FR 05-JUL-1991; 91GB-00014525.
XX
XX PA (CYTO-) CYTOCELL LTD.
XX
XX PI Cardy DLM, Delnatte SYU;
XX
XX DR WPI; 1993-045514/05.
XX
XX PT Homogeneous assay for nucleic acid sequences - obtd. by modulating enzyme
XX activity, by hybridisation of derived nucleic acid probes.
XX
XX Example 2; Page 27; 51pp; English.
XX
XX The blocker oligonucleotide p53(B) is complementary to its corresp.
XX activator probe p53(A). The oligonucleotide was synthesised with a 5'
XX bromodeoxyuridine nucleotide and may be used in an assay for the
XX detection of the human p53 anti-oncogene in human DNA. See also AAQ34750-
XX 62. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 1 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 ATGAACCGAGG 27
XX |||||
XX Db 15 ATGAACCGAGG 4
XX
XX RESULT 181
XX AAV39342/c
XX

```

ID AAV39342 standard; cDNA, 18 BP.  
 XX AAV39342;  
 AC  
 XX  
 XX 16-SEP-1998 (first entry)  
 DT  
 XX Human RAD54 mutation detecting PCR primer SEQ ID NO:50.  
 DE  
 XX Human; RAD54; cancer; xeroderma pigmentosum; Bloom syndrome;  
 KM Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily;  
 KM X-linked mental retardation with alpha-thalassemia syndrome; tumour;  
 KM gene therapy; PCR primer; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX EP844305-A2.  
 PN 27-MAY-1998.  
 PD  
 XX 10-NOV-1997; 97EP-00308998.  
 PE  
 XX 13-NOV-1996; 96US-0030676P.  
 PR  
 XX (SMK) SMITHKLINE BEECHAM CORP.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Croce CM, Fishel RA, Rasio D, Robbins DJ;  
 DR WPI; 1998-274189/25.  
 XX  
 XX Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists,  
 PT etc.  
 PS Claim 18; Page 50; 64pp; English.  
 XX  
 XX The present sequence represents a PCR primer for use in a method of the  
 CC invention for determining the genetic predisposition to cancer in an  
 CC individual by detecting hRAD54 mutations in a sample. hRAD54 is a gene  
 CC thought to be present in tumours that display allelic imbalance at 1p32,  
 CC the chromosome band identified as one of four minimal regions of  
 CC chromosome 1 deletion in breast carcinomas. hRAD54 is useful for  
 CC production of proteins, inter alia, that have been identified as novel  
 CC hRAD54 by homology between the amino acid sequence given in AA62186 and  
 CC known amino acid sequences such as yeast RAD54. hRAD54 proteins are used  
 CC in the treatment of cancer, including Xeroderma Pigmentosum and Bloom  
 CC syndrome, Werner's syndrome and X-linked mental retardation with alpha-  
 CC thalassemia syndrome and breast cancer. hRAD54 polynucleotides are also  
 CC useful for detecting complementary nucleotides for use as a diagnostic  
 CC agent, especially useful for diagnosis of disease or susceptibility to  
 CC diseases. hRAD54 polynucleotide, proteins, agonists and antagonists which  
 CC are proteins are useful in gene therapy  
 XX  
 XX Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 487 GAAGGCTGCAT 498  
 DB 12 GAAGGCTGCAT 1  
 RESULT 182  
 AA221414  
 ID AA221414 standard; DNA; 18 BP.  
 XX  
 XX AA221414;  
 AC  
 XX  
 XX 02-DEC-1999 (first entry)  
 DT  
 XX Human MEK2 antisense oligonucleotide SEQ ID NO:17.  
 DE

XX Human; MEK2; MAP kinase; MAPK/ERK kinase; erk activator kinase;  
 KM mitogen activated protein kinase; expression; modulation; antisense;  
 KM diagnosis; hepatocellular carcinoma; breast cancer; proliferation;  
 KM differentiation; development; detection; probe; primer; tumour;  
 KM phosphothiolate; ss.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX 28-SEP-1999.  
 PD  
 XX 20-NOV-1998; 98US-00197378.  
 PE  
 XX 20-NOV-1998; 98US-00197378.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 PI Monia BP, Cowsett LM;  
 DR WPI; 1999-561077/47.  
 XX  
 XX Antisense oligonucleotides of the MEK2 kinase gene, useful in diagnostic  
 PT protocols in vitro and for inhibiting the expression of MEK2 in vivo for  
 PT the treatment of human hepatocellular carcinomas and breast carcinomas.  
 XX  
 XX Claim 11; Col 39; 32pp; English.  
 PS  
 XX The present invention describes antisense oligonucleotides (asMEK2) of  
 CC the human MEK2 dual specificity kinase gene. The MEK2 gene (also called  
 CC MAPK2, mpk2, MAPK/ERK kinase 2, pmrk2 and erk activator kinase)  
 CC represents a convergent target for the regulation of a range of cellular  
 CC processes including proliferation, differentiation and development.  
 CC asMEK2 may be used to inhibit the expression of MEK2 genes in vivo and/or  
 CC in vitro. MEK2 has been shown to be over expressed in some tumour cells.  
 CC Therefore, asMEK2 may be administered to a patient to treat  
 CC hepatocellular carcinomas and breast carcinomas. asMEK2 may also be used  
 CC as a diagnostic tool to specifically inhibit the expression of MEK2  
 CC genes. The role of the inhibited genes in cellular pathways may then be  
 CC evaluated. They may also be used as probes to detect sequences encoding  
 CC MEK2 or as primers for the amplification of those sequences. AA221406 to  
 CC AA221443 represent specifically claimed asMEK2's from the present  
 CC invention  
 XX  
 XX Sequence 18 BP; 1 A; 3 C; 7 G; 7 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 130 CTGACTTTGGT 141  
 DB 6 CTGACTTTGGT 17  
 RESULT 183  
 AA231807  
 ID AA231807 standard; DNA; 18 BP.  
 XX  
 XX AA231807;  
 AC  
 XX  
 XX 24-JAN-2000 (first entry)  
 DT  
 XX Human G-alpha-13 antisense inhibitor ISIS# 20756.  
 DE  
 XX G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.  
 KM Synthetic.  
 OS Homo sapiens.  
 XX  
 XX US5981732-A.  
 PN

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XX 09-NOV-1999.
PD 04-DEC-1998; 98US-00205860.
PF 04-DEC-1998; 98US-00205860.
PR 04-DEC-1998; 98US-00205860.
XX
PA (ISIS-) ISIS PHARM INC.
PI Cowser LM;
XX WPI; 1999-633376/54.
XX
PT Antisense compound inhibiting expression of human G-alpha-13.
XX
PS Claim 11; Col 39; 38pp; English.
XX
CC This sequence represents an antisense inhibitor of the invention, and
CC inhibits the expression of the human G-alpha-13 protein. The antisense
CC compounds of the invention are of 8 to 30 nucleobases in length, that
CC inhibits the expression of the human G-alpha-13. The antisense compound
CC is useful for treating an animal, particularly humans, having or being
CC prone to a disease or condition associated with the expression of G-alpha
CC -13, such as cancer
XX
SQ Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 319 AGGATCTTCACC 330
DB 7 AGGATCTTCACC 18
XX
RESULT 184
ID AAAS2916
XX AAAS2916 standard; DNA; 18 BP.
XX
AC AAAS2916;
XX
DT 20-BP-2000 (first entry)
XX
DE Escherichia coli 055:H7 gnd gene PCR primer #8.
XX
KM Escherichia coli 055:H7; gnd; 6-phosphogluconate dehydrogenase; 6-PGD;
KM gastrointestinal infection; pathogen; 0157 lipopolysaccharide;
KM haemolytic uraemic syndrome; HUS; haemolytic anaemia; thrombocytopenia;
KM acute renal failure; polymorphism; PCR primer; ss.
XX
OS Escherichia coli.
XX
PN WO200034484-A1.
XX
PD 15-JUN-2000.
XX
PF 08-DEC-1999; 99WO-US029149.
XX
PR 08-DEC-1999; 98US-0111493P.
XX
PA (CHIL-) CHILDREN'S HOSPITAL & REGIONAL MEDICAL.
PI Tarr PI;
XX WPI; 2000-431304/37.
XX
PT New polynucleotide from Escherichia coli encoding 6-phosphogluconate
PT dehydrogenase and polymeric sequences in the nucleotide for detecting
PT strains of E. coli for diagnosis and food screening.
XX
PS Disclosure; Page 8; 84pp; English.
XX

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CC The present sequence is a PCR primer used to amplify DNA beyond the 5'
CC and 3' termini of the E. coli 055:H7 gnd gene from total genomic DNA of
CC E. coli 055:H7 strain. The resulting sequence data was used to design a
CC primer pair to amplify the E. coli 055 and allele. The gnd gene, which
CC encodes 6-phosphogluconate dehydrogenase (6-PGD), has been studied in
CC fourteen strains of E. coli. Several polymorphisms have been found that
CC can be used to identify the presence of a particular strain of E. coli
CC and/or to differentiate one strain from another. A substitution of an
CC isoleucine molecule for a threonine molecule at amino acid position 218
CC 055:H7 from less pathogenic strains of 0157:H7. E. coli 0157:H7 is an
CC extremely virulent food-borne, human pathogen that causes a spectrum of
CC diseases, including mild diarrhoea and the potentially lethal haemolytic
CC uraemic syndrome (HUS), which is defined as a triad of non-immune
CC microangiopathic haemolytic anaemia, thrombocytopenia, and acute renal
CC failure. The detection of one or more polymorphisms in 6-PGD can be used
CC to diagnose disease and to test for food or water contamination
XX
SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 186 CCGCTACATCTC 197
DB 4 CCGCTACATCTC 15
XX
RESULT 185
ID AA257673
XX AA257673 standard; DNA; 18 BP.
XX
AC AA257673;
XX
DT 05-APR-2000 (first entry)
XX
DE Human G-alpha-12 antisense inhibitor ISIS# 20661.
XX
KM G-alpha-12 inhibitor; antisense compound; cell differentiation; cancer;
KM cell growth; metastatic growth; ss; ISIS# 20661.
XX
OS Homo sapiens.
XX
PN US5998206-A.
XX
PD 07-DEC-1999.
XX
PF 23-FEB-1999; 99US-00256496.
XX
PR 23-FEB-1999; 99US-00256496.
XX
PA (ISIS-) ISIS PHARM INC.
PI Cowser LM;
XX WPI; 2000-095920/08.
XX
PT Antisense inhibition of human G-alpha-12 expression.
XX
PS Example 15; Col 36; 36pp; English.
XX
CC This is a human G-alpha-12 antisense nucleotide sequence. G-alpha-12 is a
CC member of the G12/13 subfamily of G-proteins. The primary function of G-
CC alpha-12 is in cell differentiation and growth. The invention relates to
CC antisense compounds which are 8-30 nucleotides long (see AA257668-
CC 257746). The antisense molecules are targeted to the human G-alpha-12
CC nucleic acid molecule, and inhibit the expression of G-alpha-12. The
CC molecules preferably have a modified internucleotide linkage, and at
CC least one modified sugar moiety. The compounds target different regions
CC of the human G-alpha-12 RNA. The expression of human G-alpha 12 is
CC inhibited by contacting human cells or tissues in vitro with the
CC antisense molecules. The oligonucleotides are used in modulating the

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CC function of nucleic acid molecules encoding G-alpha-12, ultimately  
 CC modulating the amount of G-alpha-12 produced. The antisense compounds can  
 CC be utilized for diagnostics, therapeutics, prophylaxis and as research  
 CC agents and kits. They may be useful in the treatment of cancer, and  
 CC metastatic growth

XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330  
 |||||  
 Db 3 AGGATCTTCACC 14

RESULT 186

AAZ44508  
 ID AAZ44508 standard; DNA; 18 BP.

AC AAZ44508;

XX 06-AUG-2003 (revised)  
 DT 07-APR-2000 (first entry)

XX Z. mais restriction fragment amplification EcoRI-primer-3.

XX Detection; forensic; restriction fragment polymorphism; multiplex PCR;  
 KM corn; primer; ss.

OS Zea mays.

PN EP969102-A2.

XX 05-JAN-2000.

XX 24-SEP-1992; 99EP-00115309.

XX 24-SEP-1991; 91EP-00402542.

XX 24-SEP-1992; 92EP-00402629.

PA (KEYG-) KEYGENE NV.

PI Zabeau M, Vos P;

XX WPI; 2000-099430/09.

XX New oligonucleotides, useful for tagging restriction fragments for  
 PT genetic diagnosis.

XX Example 4; Page 18; 42pp; English.

XX This invention describes a novel oligonucleotide (I) comprising an  
 CC adapter sequence and part of the target sequence of a restriction  
 CC endonuclease, and which has 1-10 selected nucleotides immediately  
 CC adjacent to the 3' end of the target sequence. The products of the  
 CC invention are used to tag restriction fragments which are to be amplified  
 CC by the polymerase chain reaction (PCR). This technique may be used in the  
 CC detection of restriction fragment polymorphisms (RFPs), including length  
 CC polymorphisms. The products can also be used for genetic analysis, such  
 CC as for the forensic typing of humans and the detection of the inheritance  
 CC of determined traits in animals or plants and to monitor several diseases  
 CC at once. The oligonucleotides and kits may also be used to identify  
 CC species, races or varieties of animals or plants. The new adapters,  
 CC oligonucleotides and methods for using them are more sensitive for  
 CC detecting restriction fragment polymorphisms because not only differences  
 CC in the target sites of the restriction endonuclease are detected as with  
 CC prior art methods and oligonucleotides but also differences in the  
 CC adjacent nucleotide sequences within the selective PCR primers. Multiplex  
 CC PCR may only be used to monitor 5-8 different traits simultaneously and  
 CC compromise conditions have to be established to allow all primer pairs to  
 CC yield detectable products. In addition there are strong differences in

CC the efficiency of amplification of different fragments and products of  
 CC certain primer pairs are not detectable with multiplex PCR. In contrast,  
 CC using the new techniques, all the primers have a substantial part of  
 CC their nucleotide sequence in common and by selecting Amplified Fragment  
 CC Length Polymorphisms, the DNA markers are amplified with equal  
 CC efficiency. AAZ44475-244526 represent primers used to illustrate the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX

XX Sequence 18 BP; 5 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 TTACCAATTCAA 47  
 |||||  
 Db 6 TTACCAATTCAA 17

RESULT 187

ABA92907  
 ID ABA92907 standard; DNA; 18 BP.

AC ABA92907;

XX 08-APR-2002 (first entry)

XX Angiogenin inhibitor related oligonucleotide.

XX Angiogenin inhibitor; angiogenesis; ss.

OS Synthetic.

PN KR99021167-A.

XX 25-MAR-1999.

XX 30-AUG-1997; 97KR-00044679.

XX 30-AUG-1997; 97KR-00044679.

XX (GREG) KOREA GREEN CROSS CORP.

XX (UTPO-) UNIV POHANG SCI & TECHNOLOGY.

PI Chae CB, Koh YS, Lee JE, Oh GS, Bae DG;

XX WPI; 2000-254109/22.

XX Angiogenin inhibitor.

XX Example 2; Page 6; 16pp; Korean.

XX The present invention describes angiogenin inhibitors. Angiogenin  
 CC inhibitors can be used in the treatment of angiogenesis. The present  
 CC sequence represents an oligonucleotide which is used in the  
 CC exemplification of the present invention

XX Sequence 18 BP; 2 A; 2 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 CTGTATGAGTT 558  
 |||||  
 Db 2 CTGTATGAGTT 13

RESULT 188

AAC66835  
 ID AAC66835 standard; DNA; 18 BP.

XX AAC66835;

```

XX 27-FEB-2001 (first entry)
DT
XX Human tankyrase II PCR primer gtl1-5'.
DE
XX Human; tankyrase II; telomere length; signal transduction; PCR primer;
KM ss.
XX Homo sapiens.
OS
XX MO200061813-A1.
FN
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009558.
PF
XX 09-APR-1999; 99US-0126577P.
PR 13-APR-1999; 99US-0129123P.
XX (GERO-) GERON CORP.
PA
XX Morin GB, Funk WD, Piatyarszek MA;
PI
XX WPI; 2000-679503/66.
DR
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding
PT the polypeptide useful for modulating or maintaining telomere length,
PT replicative capacity, apoptosis, chromosome packing or gene expression.
PT
XX Disclosure; Page 9; 52pp; English.
PS
XX The present invention relates to the isolation of the protein and coding
CC sequences of human tankyrase II. The tankyrase II protein is thought to
CC be involved in signal transduction in the cell, and to have binding
CC activity for other telomere-associated proteins. It is possible that it
CC plays a role in the regulation of telomere length, thus affecting the
CC replicative ability of the cell. The protein is useful for ribosylating
CC target proteins, for determining tankyrase II binding activity in a
CC sample, and for modulating telomere length in a cell. The present
CC sequence is a PCR primer used in the isolation of the tankyrase II coding
CC sequence
SQ
SQ Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14
RESULT 189
AAH47521
ID AAH47521 standard; DNA; 18 BP.
AC AAH47521;
XX
XX 30-NOV-2001 (first entry)
DT
XX Human MMP-8 cDNA amplifying sense primer E.
DE
XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
KM anti-arthritis; cytostatic; anti-Parkinsonian; neuroprotective;
KM neutropenic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
KM Huntington's disease; human; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX US1973-H.
XX
XX 03-UTL-2001.

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XX 22-OCT-1998; 98US-00178002.
PF
XX 22-OCT-1998; 98US-00178002.
PR
XX (NOVS) NOVARTIS AG.
PA
XX Hu S;
PI
XX WPI; 2001-431511/46.
DR
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents
PT and materials for discovering treatments and diagnostics to human
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.
PT
XX Example 1; Col 25; 25pp; English.
PS
XX The invention relates to human MMP-8alt polypeptide and polynucleotides.
CC MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)
CC cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant
CC methodology. The polynucleotides and polypeptides may be used as research
CC reagents and materials for the discovery of treatments and diagnostics to
CC human disease, and as targets for identifying modulators. Inhibitors of
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's
CC disease and Huntington's disease. Sequences AAH47517-21 represent PCR
CC primers for cDNA and genomic DNA cloning of MMP-8alt
CC
XX Sequence 18 BP; 7 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
SQ
SQ
Query Match 2.0%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 94 GTAGTGAGAGG 105
Db 6 GTAGTGAGAGG 17
RESULT 190
AAC99241
ID AAC99241 standard; DNA; 18 BP.
AC AAC99241;
XX
XX 06-MAR-2001 (first entry)
DT
XX Probe sequence used in probe array SEQ ID 1.
DE
XX Probe; probe array; probe-combined substrate; detection; ss.
XX
XX Synthetic.
OS
XX JF2000270896-A.
FN
XX 03-OCT-2000.
PD
XX 28-JAN-1999; 99UP-00019915.
PF
XX 28-JAN-1999; 99UP-00019915.
PR
XX (CANO) CANON KK.
PA
XX WPI; 2001-027424/04.
DR
XX A preparation of a probe-combined substrate, a probe array, detection of
PT a target substance, specification of the base sequence of a single-
PT stranded nucleic acid in a sample, and determination of a target
PT substance in a sample.
PT
XX Example 3; Page 11; 20pp; Japanese.
PS

```

CC This invention relates to a probe-combined substrate, a probe array, and  
 CC a method for the detection of a target substance in a sample. The probe  
 CC array can be used for detecting a target substance with high reliability.  
 CC Sequences AAC99241 - AAC99305 represent probes used in an array in an  
 CC example illustrating the invention

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27  
 |||||  
 1 ATGAACCGGAGG 12

RESULT 191  
 AAC99283/C  
 ID AAC99283 standard; DNA; 18 BP.

XX AAC99283;

DT 06-MAR-2001 (first entry)

DE Probe sequence used in probe array SEQ ID 43.

KM Probe; probe array; probe-combined substrate; detection; ss.

OS Synthetic.

XX JP2000270896-A.

XX 03-OCT-2000.

XX 28-JAN-1999; 99UP-00019915.

XX 28-JAN-1999; 99UP-00019915.

XX (CANO) CANON KK.

DR WPI; 2001-027424/04.

PT A preparation of a probe-combined substrate, a probe array, detection of  
 PT a target substance, specification of the base sequence of a single-  
 PT stranded nucleic acid in a sample, and determination of a target  
 PT substance in a sample.

PS Example 3; Page 17; 20pp; Japanese.

CC This invention relates to a probe-combined substrate, a probe array, and  
 CC a method for the detection of a target substance in a sample. The probe  
 CC array can be used for detecting a target substance with high reliability.  
 CC Sequences AAC99241 - AAC99305 represent probes used in an array in an  
 CC example illustrating the invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27  
 |||||  
 18 ATGAACCGGAGG 7

RESULT 192

AAC91122  
 ID AAC91122 standard; DNA; 18 BP.

XX AAC91122;

XX

DT 20-MAR-2001 (first entry)

XX Fungal pathogenic species identification probe #8.

DE Fungal pathogenic; Internal Transcribed Spacer; ITS;

KM Opportunistic infection; ss.

XX Unidentified.

XX WO20007349-A2.

XX 07-DEC-2000.

XX 24-MAY-2000; 2000WO-EP004714.

XX 28-MAY-1999; 99EP-00870109.

XX 11-JUN-1999; 99US-0138621P.

XX (INNO-) INNOGENETICS NV.

PA (IRBI-) ENTERPRISE IRELAND T/A BIORESEARCH IRELA.

PI Smith T, Maher M, Martin C, James G, Rossau R, Van Der Weide M;

DR WPI; 2001-061555/07.

PT Detecting and identifying fungal pathogens, especially *Candida*,  
 PT *Cryptococcus* and *Aspergillus*, comprises hybridizing the amplified nucleic  
 PT acid of the fungal pathogen with a probe from the internal transcribed  
 PT spacer region of a DNA.

XX Claim 1; Page 46; 59pp; English.

CC The present invention relates to detecting and identifying fungal  
 CC pathogenic species in a sample. The method involves hybridizing a nucleic  
 CC acid of a fungal pathogen possibly present in the sample with at least  
 CC one oligonucleotide probe, from an internal Transcribed Spacer (ITS)  
 CC region. The method is useful for simultaneous detection and  
 CC differentiation of clinically important fungi in a single assay,  
 CC particularly *Candida albicans*, *C. parapsilosis*, *C. tropicalis*, *C. kefyr*,  
 CC *C. krusei*, *C. glabrata*, *C. dubliniensis*, *Aspergillus flavus*, *A.*  
 CC *versicole*, *A. nidulans*, *A. fumigatus*, *C. neoformans* and *pneumocystis*  
 CC *carinii*. The method is especially useful in the detection of  
 CC opportunistic infections in patients with impaired immunity systems, such  
 CC as organ transplant patients, patients receiving intensive anticancer  
 CC treatments, diabetics or AIDS patients

XX Sequence 18 BP; 3 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
 |||||  
 6 TCGTCTCTCCAG 17

RESULT 193

ABK72521  
 ID ABK72521 standard; DNA; 18 BP.

XX ABK72521;

DT 13-AUG-2002 (first entry)

DE DNA sequence #19 relating to nucleic acid base sequence analysis method.

XX Nucleic acid base sequence analysis; DNA diagnosis; ds.

XX Synthetic.

XX WO200233068-A1.

XX

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PD      25-APR-2002.
PE      18-OCT-2000; 2000MO-JP007244.
PF      18-OCT-2000; 2000MO-JP007244.
PR      18-OCT-2000; 2000MO-JP007244.
PS      (CANO ) CANON KK.
PT      Yamamoto N, Okamoto T, Suzuki T;
DR      WPI; 2002-372310/40.
XX      Screening an unknown base sequence at a defined site of a target single-stranded nucleic acid for use in DNA diagnosis and therapy, comprises a DNA chip, fluorescence yield and pattern-based method.
XX      Disclosure; Page 8; 53pp; Japanese.
CC      The present invention relates to a method of analysing an unknown nucleic acid base sequence. The method comprises preparing a probe array, hybridising with the probe array, measuring the fluorescence yield in the reaction, obtaining a template pattern, producing a sample pattern, and comparing the sample pattern with the template pattern. The method is useful for specifying an unknown base sequence at a defined site of a target single-stranded nucleic acid, which is useful for analysing a therapeutic acid base sequence. The method is applicable in DNA diagnosis and therapy, and is useful in medicine and biology. Measuring the fluorescence yield allows the detection of a one-base mismatch which can be considered to produce high detection accuracy. The hybrid pattern of the DNA probe is used so the difference in thermostability is less important, and the judgement on each spot can be reliably carried out. ABK72503-ABK72524 represent DNA sequences described in the specification of the present invention
SQ      Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY      16 ATGACCGGAGC 27
        |||
        1 ATGACCGGAGC 12

RESULT 194
ID      ABRK72480/c
XX      ABRK72480 standard; DNA; 18 BP.
AC      ABRK72480;
DT      13-AUG-2002 (first entry)
DE      Sample origin/nucleotide #42 for analysing nucleic acid base sequence.
KW      Nucleic acid base sequence analysis; DNA diagnosis; probe; ss.
OS      Synthetic.
PN      WO200233068-A1.
PD      25-APR-2002.
PE      18-OCT-2000; 2000MO-JP007244.
PR      18-OCT-2000; 2000MO-JP007244.
PS      (CANO ) CANON KK.
PT      Yamamoto N, Okamoto T, Suzuki T;
DR      WPI; 2002-372310/40.
XX      Screening an unknown base sequence at a defined site of a target single-stranded nucleic acid for use in DNA diagnosis and therapy, comprises a DNA chip, fluorescence yield and pattern-based method.
XX      Disclosure; Page 8; 53pp; Japanese.
CC      The present invention relates to a method of analysing an unknown nucleic acid base sequence. The method comprises preparing a probe array, hybridising with the probe array, measuring the fluorescence yield in the reaction, obtaining a template pattern, producing a sample pattern, and comparing the sample pattern with the template pattern. The method is useful for specifying an unknown base sequence at a defined site of a target single-stranded nucleic acid, which is useful for analysing a therapeutic acid base sequence. The method is applicable in DNA diagnosis and therapy, and is useful in medicine and biology. Measuring the fluorescence yield allows the detection of a one-base mismatch which can be considered to produce high detection accuracy. The hybrid pattern of the DNA probe is used so the difference in thermostability is less important, and the judgement on each spot can be reliably carried out. ABK72503-ABK72524 represent DNA sequences described in the specification of the present invention
SQ      Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY      16 ATGACCGGAGC 27
        |||
        1 ATGACCGGAGC 12

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PT Screening an unknown base sequence at a defined site of a target single-
PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
PT DNA chip, fluorescence yield and pattern-based method.
XX
XX Example 1; Page 13; 53pp; Japanese.
PS
XX The present invention relates to a method of analysing an unknown nucleic
XX acid base sequence. The method comprises preparing a probe array,
CC hybridising with the probe array, measuring the fluorescence yield in the
CC reaction, obtaining a template pattern, producing a sample pattern, and
CC comparing the sample pattern with the template pattern. The method is
CC useful for specifying an unknown base sequence at a defined site of a
CC target single-stranded nucleic acid, which is useful for analysing a
CC nucleic acid base sequence. The method is applicable in DNA diagnosis and
CC therapy, and is useful in medicine and biology. Measuring the
CC fluorescence yield allows the detection of a one-base mismatch which can
CC be considered to produce high detection accuracy. The hybrid pattern of
CC the DNA probe is used so the difference in thermostability is less
CC important, and the judgement on each spot can be reliably carried out.
CC ABK72439-ABK72502 represent sample originucleotides used in the present
CC invention
CC
SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ATGAACCGGAGG 27
   |||||
Db 18 ATGAACCGGAGG 7

RESULT 195
ID ABK72522/C
AC ABK72522;
XX
XX 13-AUG-2002 (first entry)
DT
XX
DE DNA sequence #20 relating to nucleic acid base sequence analysis method.
XX
XX Nucleic acid base sequence analysis; DNA diagnosis; ds.
XX
XX Synthetic.
XX
XX WO200233068-A1.
XX
XX 25-APR-2002.
XX
XX 18-OCT-2000; 2000WO-JP007244.
XX
XX 18-OCT-2000; 2000WO-JP007244.
XX
XX (CANO ) CANON KK.
XX
XX Yamamoto N, Okamoto T, Suzuki T;
XX
XX WPI; 2002-372310/40.
XX
XX Screening an unknown base sequence at a defined site of a target single-
PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
PT DNA chip, fluorescence yield and pattern-based method.
PS
PS Disclosure, Page 8; 53pp; Japanese.
XX
XX The present invention relates to a method of analysing an unknown nucleic
XX acid base sequence. The method comprises preparing a probe array,
CC hybridising with the probe array, measuring the fluorescence yield in the
CC reaction, obtaining a template pattern, producing a sample pattern, and
CC comparing the sample pattern with the template pattern. The method is
CC useful for specifying an unknown base sequence at a defined site of a

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CC target single-stranded nucleic acid, which is useful for analysing a  
 CC nucleic acid base sequence. The method is applicable in DNA diagnosis and  
 CC therapy, and is useful in medicine and biology. Measuring the  
 CC fluorescence yield allows the detection of a one-base mismatch which can  
 CC be considered to produce high detection accuracy. The hybrid pattern of  
 CC the DNA probe is used so the difference in thermostability is less  
 CC important, and the judgement on each spot can be reliably carried out.  
 CC ABK72503-ABK72524 represent DNA sequences described in the specification  
 CC of the present invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27

Db 18 ATGAACCGGAGG 7

RESULT 196

ABN99788/c

ID ABN99788 standard; DNA; 18 BP.

XX ABN99788;

AC ABN99788;

DT 20-AUG-2002 (first entry)

DE DNA probe #42 for use in an oligonucleotide array.

XX Human; probe; array; oligonucleotide detection; ss.

XX Synthetic.

XX JP2002065274-A.

XX 05-MAR-2002.

XX 31-AUG-2000; 2000JP-00263395.

XX 31-AUG-2000; 2000JP-00263395.

XX (CANO) CANON KK.

XX WPI; 2002-474139/51.

XX Detection of an object component in a sample using an oligonucleotide as  
 PT detecting probe.

XX Example 3; Page 19; 25pp; Japanese.

XX The invention relates to a novel method for detecting a complex formed  
 CC between a probe and its complement. The method is used for detecting a  
 CC complex formed between an oligonucleotide of known base sequence and a  
 CC complementary probe, and for evaluating if the sequence is contained in  
 CC liquid samples, or the level of binding by using the oligonucleotide as  
 CC the detecting probe. The sequence represents a probe used in the  
 CC invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27

Db 18 ATGAACCGGAGG 7

RESULT 197

ABL54942/c

ID ABL54942 standard; DNA; 18 BP.

XX ABL54942;

AC 18-JUN-2002 (first entry)

DE Human tumour suppressor gene p53 probe #42.

XX Human; p53; probe; variation detection; DNA array; ss.

XX Homo sapiens.

XX EPI184467-A2.

XX 06-MAR-2002.

XX 31-AUG-2001; 2001EP-00307415.

XX 31-AUG-2000; 2000JP-00263396.

XX (CANO) CANON KK.

XX Yamamoto N, Okamoto T, Tanaka S, Suzuki T;

XX WPI; 2002-271043/32.

XX Screening for gene variation by using DNA array in which probes giving  
 FT strong signals forming hybrids with normal sequence, and probes having  
 PT sequences expected to form hybrids with variants are separately arranged.

XX Example 2; Page 6; 22pp; English.

XX The sequence represents a full match probe designed to detect a variation  
 CC a specific base in the p53 gene sequence. The invention relates to a  
 CC novel method for screening for a variation in a nucleic acid sequence.  
 CC The method involves using a DNA array in which a group of probes which  
 CC will give strong signals forming hybrids with a normal gene sequence, and  
 CC a group of probes having sequences expected to form hybrids with gene  
 CC variants are separately arranged. The method is useful for screening for  
 CC the presence or absence of variation in a nucleic acid sequence. The  
 CC method is also useful for mass screening to determine rapidly the  
 CC presence or absence of a gene variation without need of an expensive  
 CC apparatus and a complex analysis

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 6; Length 18;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27

Db 18 ATGAACCGGAGG 7

RESULT 198

ABL54965

ID ABL54965 standard; DNA; 18 BP.

XX ABL54965;

XX 18-JUN-2002 (first entry)

DE Human rhodamine labelled p53 gene fragment #65 (normal sequence).

XX Human; p53; rhodamine; variation detection; DNA array; ss.

XX Homo sapiens.

XX Key modified\_base 1 Location/Qualifiers

FT /\*tag= a

FT /note= "Rhodamine labelled"

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XX      EPI184467-A2.
XX      PD
XX      06-MAR-2002.
XX      PF
XX      31-AUG-2001; 2001EP-00307415.
XX      PR
XX      31-AUG-2000; 2000JP-00263396.
XX      PA
XX      (CANO ) CANON KK.
XX      PI
XX      Yamamoto N, Okamoto T, Tanaka S, Suzuki T,
XX      DR
XX      WPI; 2002-271043/32.
XX      PT
XX      Screening for gene variation by using DNA array in which probes giving
XX      PT strong signals forming hybrids with normal sequence, and probes having
XX      PT sequences expected to form hybrids with variants are separately arranged.
XX      CC
XX      Example 2; Page 9; 22pp; English.
XX      CC
XX      The sequence represents a section of the normal p53 gene, designated DNA
XX      CC #65. The sequence was used as a target for hybridisation in the
XX      CC invention, and hybridises to probe #42. The invention relates to a novel
XX      CC method for screening for a variation in a nucleic acid sequence. The
XX      CC method involves using a DNA array in which a group of probes which will
XX      CC give strong signals forming hybrids with a normal gene sequence, and a
XX      CC group of probes having sequences expected to form hybrids with gene
XX      CC variants are separately arranged. The method is useful for screening for
XX      CC the presence or absence of variation in a nucleic acid sequence. The
XX      CC method is also useful for mass screening to determine rapidly the
XX      CC presence or absence of a gene variation without need of an expensive
XX      CC apparatus and a complex analysis
XX      CC
XX      SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      2.0%; Score 12; DB 6; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      16 ATGAACCGGAGG 27
XX      DB      1 ATGAACCGGAGG 12
XX
XX      RESULT 199
XX      ABL58276
XX      ID ABL58276 standard; DNA; 18 BP.
XX      AC
XX      ABL58276;
XX      DT
XX      15-JUL-2002 (first entry)
XX      DE
XX      Base oligonucleotide for preparation of a probe.
XX      KM
XX      Liquid discharge; nucleic acid analysis; gene examination; probe; ss.
XX      OS
XX      Synthetic.
XX      XX
XX      EPI188475-A2.
XX      PD
XX      20-MAR-2002.
XX      PF
XX      18-SEP-2001; 2001EP-00307932.
XX      PR
XX      19-SEP-2000; 2000JP-00284046.
XX      PR
XX      19-FEB-2001; 2001JP-00042344.
XX      XX
XX      (CANO ) CANON KK.
XX      PA
XX      Okamoto T, Yamamoto N, Watanabe H, Suzuki T,
XX      PI
XX      WPI; 2002-364388/40.

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XX      XX
XX      Producing probe supports for use in base sequence analysis of gene
XX      PT deoxyribonucleic acid, involves providing liquid discharging device for
XX      PT two-dimensionally arranging and fixing probe arrays on solid-phase
XX      PT substrates.
XX      CC
XX      Disclosure; Page 20; 53pp; English.
XX      PS
XX      The invention relates to producing a probe support. The method involves
XX      CC (a) providing a liquid discharging device including reservoirs for
XX      CC containing liquids containing the probes and discharge nozzles connecting
XX      CC with the corresponding reservoirs; (b) aligning the liquid discharging nozzles and
XX      CC the support relatively; and (c) discharging the liquids containing the
XX      CC probes from the discharge nozzles to different positions on the support.
XX      CC The number of reservoirs and discharge nozzles are the number of probes.
XX      CC The method is useful for producing probe supports useful in base sequence
XX      CC analysis of gene deoxyribonucleic acid (DNAs) and gene examination. The
XX      CC present sequence represents a base oligonucleotide used for preparation
XX      CC of a probe
XX      CC
XX      SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      2.0%; Score 12; DB 6; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      16 ATGAACCGGAGG 27
XX      DB      1 ATGAACCGGAGG 12
XX
XX      RESULT 200
XX      ABL58543
XX      ID ABL58543 standard; DNA; 18 BP.
XX      AC
XX      ABL58543;
XX      DT
XX      07-OCT-2002 (first entry)
XX      DE
XX      Synthetic hybridisation probe for nucleic acid detection method.
XX      KM
XX      Probe nucleic acid; target nucleic acid; hybrid; nucleic acid detection;
XX      KM ss.
XX      OS
XX      Synthetic.
XX      XX
XX      JP2002176999-A.
XX      PN
XX      25-JUN-2002.
XX      PD
XX      12-DEC-2000; 2000JP-00377349.
XX      PF
XX      12-DEC-2000; 2000JP-00377349.
XX      PR
XX      12-DEC-2000; 2000JP-00377349.
XX      XX
XX      (CANO ) CANON KK.
XX      PA
XX      WPI; 2002-569947/61.
XX      DR
XX      Detecting nucleic acid with hybrid formation of a probe nucleic acid and
XX      PT a target nucleic acid without interference of the other double stranded
XX      PT nucleic molecules.
XX      CC
XX      Example 1; Page 9; 13pp; Japanese.
XX      PS
XX      The invention describes a hybrid of a probe nucleic acid and a target
XX      CC nucleic acid for detection of nucleic acid. This sequence represents a
XX      CC synthetic hybridisation probe used in the nucleic acid detection method of
XX      CC the invention
XX      CC
XX      SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      2.0%; Score 12; DB 6; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 1.2e+05;

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
 XX |||||  
 DB 1 ATGACCGGAGG 12

RESULT 201  
 ABR8542/c  
 ID ABR8542 standard; DNA; 18 BP.  
 XX  
 AC ABR8542;  
 XX  
 XX 07-OCT-2002 (first entry)  
 DT  
 XX  
 DE Synthetic target gene fragment for nucleic acid detection method #1.  
 XX  
 KW Probe nucleic acid; target nucleic acid; hybrid; nucleic acid detection;  
 XX ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2002176999-A.  
 XX  
 PD 25-JUN-2002.  
 XX  
 PF 12-DEC-2000; 2000JP-00377349.  
 XX  
 PR 12-DEC-2000; 2000JP-00377349.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2002-569947/61.  
 XX

PT Detecting nucleic acid with hybrid formation of a probe nucleic acid and  
 a target nucleic acid without interference of the other double stranded  
 PT nucleic molecules.  
 XX  
 PS Example 1; Page 9; 13pp; Japanese.  
 XX  
 CC The invention describes a hybrid of a probe nucleic acid and a target  
 CC nucleic acid for detection of nucleic acid. This sequence represents a  
 CC synthetic target gene fragment for probe hybridisation used in the nucleic  
 CC acid detection method of the invention  
 XX

SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
 XX |||||  
 DB 18 ATGACCGGAGG 7

RESULT 202  
 ABR04735/c  
 ID ABR04735 standard; DNA; 18 BP.  
 XX  
 AC ABR04735;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE End-labelled probe array production method-related oligonucleotide 42.  
 XX  
 KW End-labelled probe array production; probe; ss; target substance capture.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2002153284-A.  
 XX  
 PD 28-MAY-2002.

XX 24-NOV-2000; 2000JP-00357446.  
 PF  
 PR 24-NOV-2000; 2000JP-00357446.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2002-552742/59.  
 XX  
 PT Preparation of an end-labelled probe array, for capturing a target  
 PT substance.  
 XX  
 PS Example 1; Page 5; 25pp; Japanese.  
 XX  
 CC The invention comprises a method for the synthesis of an end-labelled  
 CC probe array - in which part of a probe for capturing a target substance  
 CC is fixed at a plural of the matrix sites on the surface of a probe array  
 CC substrate. In the method of the invention the units for constituting the  
 CC probe are combined successively and, at the final stage of the successive  
 CC synthesis, a labelling substance is combined to the end of the probe and  
 CC extended to a desired chain length. The method of the invention is useful  
 CC for the production of a probe array. The present DNA sequence represents  
 CC an oligonucleotide that was used in an example of the invention  
 XX  
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27  
 XX |||||  
 DB 18 ATGACCGGAGG 7

RESULT 203  
 ABR04758  
 ID ABR04758 standard; DNA; 18 BP.  
 XX  
 AC ABR04758;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE End-labelled probe array production method-related oligonucleotide 65.  
 XX  
 KW End-labelled probe array production; probe; ss; target substance capture.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2002153284-A.  
 XX  
 PD 28-MAY-2002.  
 XX  
 PF 24-NOV-2000; 2000JP-00357446.  
 XX  
 PR 24-NOV-2000; 2000JP-00357446.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2002-552742/59.  
 XX  
 PT Preparation of an end-labelled probe array, for capturing a target  
 PT substance.  
 XX  
 PS Example 1; Fig 1; 25pp; Japanese.  
 XX  
 CC The invention comprises a method for the synthesis of an end-labelled  
 CC probe array - in which part of a probe for capturing a target substance  
 CC is fixed at a plural of the matrix sites on the surface of a probe array  
 CC substrate. In the method of the invention the units for constituting the  
 CC probe are combined successively and, at the final stage of the successive  
 CC synthesis, a labelling substance is combined to the end of the probe and  
 CC extended to a desired chain length. The method of the invention is useful

CC for the production of a probe array. The present DNA sequence represents  
CC an oligonucleotide that was used in an example of the invention

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27

Db 1 ATGAACCGGAGG 12

RESULT 204

ABQ81304/c

ID ABQ81304 standard; DNA; 18 BP.

XX ABQ81304;

XX 12-DEC-2002 (first entry)

DE Cytochrome P450 CYP2A6 sense primer.

XX Cytochrome P450; CYP2A6; enzyme; tachyphylaxis; drug tolerance; human;

KM psoriasis; antipsoriatic; antipruritic; dermatological; PCR; primer; ss.

XX Homo sapiens.

XX WO200245704-A2.

XX 13-JUN-2002.

PF 04-DEC-2001; 2001WO-GB005369.

XX 04-DEC-2000; 2000GB-00029524.

XX (MOLE-) MOLECULAR SKINCARE LTD.

PI Adcocks C, Bavić C, Cork M, Duff G, Tazi-Ahmini R, Ward S;

DR WPI; 2002-713334/77.

PT Alleviating or preventing a tachyphylactic response to an agent and  
PT treating psoriasis, comprises administering an antagonist of a metabolic  
PT enzyme, which is induced as a result of exposure to the agent, to a  
PT patient.

PS Example 1; Page 75; 136pp; English.

XX The present sequence is a sense primer for cytochrome P450 CYP2A6. RT-PCR  
CC was used to characterise metabolic enzyme induction by vitamin D  
CC analogues, corticosteroids and macrobiacams in human skin. The invention  
CC provides for the use of antagonists of P450 enzymes for the prevention or  
CC alleviation of a tachyphylactic response to administration of a vitamin D  
CC analogue, corticosteroid or macrobiaccam to a patient, e.g. for the  
CC treatment of psoriasis. The underlying cause of tachyphylaxis was shown  
CC to be degradation of a drug in the patient, rather than desensitization  
CC or receptor down-regulation. Exposure of a patient to the drug for  
CC extended periods results in an increase in the expression of enzymes  
CC which are capable of metabolizing the drug. A method for treatment of  
CC tachyphylaxis therefore involves inhibiting the induced metabolic enzyme,  
CC especially a P450 cytochrome, by administration of an antagonist of the  
CC enzyme. Detection of an increase in the amount and/or activity of a  
CC metabolic enzyme capable of metabolizing a drug following extended  
CC exposure of a cell from an individual to the drug indicates the increased  
CC likelihood of that individual developing a tachyphylactic response to the  
CC drug

XX Sequence 18 BP; 8 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCTC 186

Db 16 TTGCTCTTCTC 5

RESULT 205

ABL59677/c

ID ABL59677 standard; DNA; 18 BP.

XX ABL59677;

XX 18-JUL-2002 (first entry)

DE Oligonucleotide probe SEQ ID NO:42.

XX Simultaneous determination; probe; ss.

XX Synthetic.

XX JP2002065299-A.

XX 05-MAR-2002.

PD 31-AUG-2000; 2000JP-00263505.

XX 31-AUG-2000; 2000JP-00263505.

XX (CANO) CANON KK.

XX WPI; 2002-398978/43.

XX Simultaneous testing of the reactivity of a sample with other different  
PT samples, comprises applying to the two samples to a substrate comprising  
PT divided matrices.

XX Example 1; Page 11; 24pp; Japanese.

XX The present invention describes a method for determining simultaneously  
CC the reactivity of a first sample with other samples, in which the second  
CC to the 2 plus nth (n is not less than 1) samples having different  
CC properties are arranged independently on a substrate, on whose surface  
CC the first sample is already present, and the reactivities between the  
CC first sample and each of the second to the 2 plus n-th samples are  
CC determined. Also described is a tissue sample matrix in which several  
CC samples from different sources are present on each matrix divided on a  
CC substrate. The method is used for determining simultaneously the  
CC reactivity of a first sample with several other differing samples.

CC ABL59636 to ABL59701 represent oligonucleotide probes used in an example  
CC from the present invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27

Db 18 ATGAACCGGAGG 7

RESULT 206

ABT06256/c

ID ABT06256 standard; DNA; 18 BP.

XX ABT06256;

XX 24-OCT-2002 (first entry)

DE Synthetic DNA selling system - related oligonucleotide 61.

KW synthetic DNA selling system; internet; ss; purchase order menu;  
 XX major histocompatibility complex; MHC.  
 OS Synthetic.  
 PN JP2002074089-A.  
 XX  
 PD 12-MAR-2002.  
 XX  
 PF 29-AUG-2000; 2000JP-00259715.  
 XX  
 PR 29-AUG-2000; 2000JP-00259715.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2002-492955/53.  
 XX  
 PT Synthetic DNA selling system using the internet; displays purchase order  
 PT menu to orderer's terminal and initiates production of selected DNA for  
 PT the successful bidder.  
 XX  
 PS Disclosure; Fig 5; 22pp; Japanese.  
 XX  
 CC The invention comprises a synthetic DNA selling system using the  
 CC internet. The system displays a purchase order menu display, with the  
 CC number of base sequences of DNA from which the orderer selects a DNA. The  
 CC order information is transmitted to a successful bidder side server which  
 CC orders for production and delivery of selected synthetic DNA. The system  
 CC of the invention is useful for marketing synthetic DNAs of different base  
 CC sequences and concentrations according to the desire of the user,  
 CC especially genes concerned with human major histocompatibility complex  
 CC (MHC). Oligonucleotides ABR06196 - ABR06278 are used in the invention  
 XX  
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 6; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 ATGACCGGAGG 27  
 DB 18 ATGACCGGAGG 7  
 XX  
 RESULT 207  
 ID AAD51874  
 XX AAD51874 standard; DNA; 18 BP.  
 XX  
 AC AAD51874;  
 XX  
 DT 02-MAY-2003 (first entry)  
 XX  
 DE Porcine interferon (IFN)-alpha DNA amplifying forward PCR primer.  
 XX  
 KM Porcine; interferon; IFN; foot and mouth disease; vaccine; immunisation;  
 KM FMD; virucide; PCR; primer; ss.  
 XX  
 OS Sus sp.  
 OS  
 PN WO200287336-A1.  
 XX  
 PD 07-NOV-2002.  
 XX  
 PF 26-APR-2002; 2002WO-US012247.  
 XX  
 PR 26-APR-2001; 2001US-0286345P.  
 PR 24-APR-2002; 2002US-00128463.  
 XX  
 PA (USDA ) US SEC OF AGRIC.  
 XX  
 PI Grubman MJ, Chinsangara J, Koester M, Moraes MP;  
 XX WPI; 2003-140146/13.

XX  
 XX New construct comprising a DNA sequence capable of expressing interferon  
 PT in animals susceptible to foot and mouth disease, useful for preparing a  
 PT vaccine for providing protective immunization against foot and mouth  
 PT disease.  
 XX  
 PS Example 3; Page 71; 72pp; English.  
 XX  
 CC The invention relates to a novel construct comprising a DNA sequence  
 CC capable of expressing interferon (IFN) in animals susceptible to foot and  
 CC mouth disease (FMD). The construct, vaccine and method are useful for  
 CC protective immunisation against foot and mouth disease in animals. The  
 CC construct is useful for preparing a vaccine, which is particularly useful  
 CC for stimulating protective response to such disease. The present sequence  
 CC is porcine interferon (pIFN)-alpha DNA amplifying PCR primer. This  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 18 BP; 4 A; 9 C; 3 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 303 CCCCAACTCAG 314  
 DB 5 CCCCAACTCAG 16  
 XX  
 RESULT 208  
 ID AB221481  
 XX AB221481 standard; DNA; 18 BP.  
 XX  
 AC AB221481;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE Synthetic probe SEQ ID NO 1.  
 XX  
 KM Probe array; probe; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN JP2002253251-A.  
 XX  
 PD 10-SEP-2002.  
 XX  
 PF 28-FEB-2001; 2001JP-00055972.  
 XX  
 PR 28-FEB-2001; 2001JP-00055972.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2003-096532/09.  
 XX  
 PT A process for preparation of a high density array of probes, used for DNA  
 PT analysis and screening, comprising solution dropped on a carrier to form  
 PT multiple spots at high speed.  
 XX  
 PS Example 3; Page 12; 19pp; Japanese.  
 XX  
 CC The invention relates to preparation of a probe array by high speed and  
 CC accurate dropping of the probe solution to improve quality of the probe  
 CC array. The probe array is useful in the analysis of base sequences of DNA  
 CC and reliable genetic screening of multiple items. The present sequence is  
 CC that of a probe used in examples of the invention  
 XX  
 SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 ATGACCGGAGG 27

Db 1 ATGAACCGAGG 12

RESULT 209  
AB221482/C  
ID AB221482 standard; DNA; 18 BP.

AC AB221482;

DT 28-MAR-2003 (first entry)

DE Synthetic probe SEQ ID NO 2.

XX Probe array; probe; ss.

OS Synthetic.

XX Key Location/Qualifiers  
FH modified\_base 1

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "G-OP03-(CH2)6-SH"

XX JP2002253251-A.

XX 10-SEP-2002.

XX 28-FEB-2001; 2001JP-00055972.

XX 28-FEB-2001; 2001JP-00055972.

XX (CANO ) CANON KK.

XX WPI; 2003-096532/09.

XX A process for preparation of a high density array of probes, used for DNA  
PT analysis and screening, comprising solution dropped on a carrier to form  
PT multiple spots at high speed.

XX Example 3; Page 12; 19pp; Japanese.

XX The invention relates to preparation of a probe array by high speed and  
CC accurate dropping of the probe solution to improve quality of the probe  
CC array. The probe array is useful in the analysis of base sequences of DNA  
CC and reliable genetic screening of multiple items. The present sequence is  
CC that of a probe used in examples of the invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 7; Length 18;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27  
DB 18 ATGAACCGAGG 7

RESULT 210

ABV77868  
ID ABV77868 standard; DNA; 18 BP.

AC ABV77868;

DT 24-FEB-2003 (first entry)

DE Oligonucleotide SEQ ID 1 used to prepare a probe.

XX Probe; probe carrier; DNA micro-chip; ss.

OS Synthetic.

FH Key Location/Qualifiers  
FT modified\_base 1  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "5' labelled with tetramethyl rhodamine"

XX JP2002257694-A.

XX 11-SEP-2002.

XX 28-FEB-2001; 2001JP-00055970.

XX 28-FEB-2001; 2001JP-00055970.

XX (CANO ) CANON KK.

XX WPI; 2003-079066/08.

XX Device for manufacturing a probe carrier used for analyzing base sequence  
PT of genetic DNA comprises discharging liquid through a group of  
PT discharging openings on each probe spot.

XX Example 4; Page 12; 18pp; Japanese.

XX The present invention relates to a device for manufacturing a probe  
CC carrier with some types of probes. The device comprises: (i) a solution  
CC discharge unit composed of reservoirs for housing the respective types of  
CC probe solutions; (ii) groups of discharging openings connected to the  
CC respective reservoirs; and (iii) discharging energy generating members  
CC corresponding to the respective discharging openings one by one. The  
CC device is suitable for manufacturing probe carriers, such as, DNA micro-  
CC chips etc. used for analysing base sequence of genetic DNA etc. The  
CC present sequence is a oligonucleotide used for preparing a probe, which  
CC was used in an example from the invention

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 7; Length 18;  
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27  
DB 1 ATGAACCGAGG 12

RESULT 211

ABV77869/C  
ID ABV77869 standard; DNA; 18 BP.

AC ABV77869;

DT 24-FEB-2003 (first entry)

DE Oligonucleotide SEQ ID 2 used to prepare a probe.

XX Probe; probe carrier; DNA micro-chip; ss.

OS Synthetic.

XX Key Location/Qualifiers  
FH modified\_base 1

FT /\*tag= a

FT /mod\_base= OTHER

FT /note= "5' labelled with SH-(CH2)6-PO4"

XX JP2002257694-A.

XX 11-SEP-2002.

XX 28-FEB-2001; 2001JP-00055970.

XX (CANO ) CANON KK.  
 PA WPI; 2003-079066/08.  
 XX  
 DR  
 XX  
 PT Device for manufacturing a probe carrier used for analyzing base sequence  
 PT of genetic DNA comprises discharging liquid through a group of  
 PT discharging openings on each probe spot.  
 XX  
 PS Example 4; Page 12; 18pp; Japanese.  
 XX  
 CC The present invention relates to a device for manufacturing a probe  
 CC carrier with some types of probes. The device comprises: (i) a solution  
 CC discharge unit composed of reservoirs for housing the respective types of  
 CC probe solutions; (ii) groups of discharging openings connected to the  
 CC respective reservoirs; and (iii) discharging energy generating members  
 CC corresponding to the respective discharging openings one by one. The  
 CC device is suitable for manufacturing probe carriers, such as, DNA micro-  
 CC chips etc. used for analyzing base sequence of genetic DNA etc. The  
 CC present sequence is a oligonucleotide used for preparing a probe, which  
 CC was used in an example from the invention. Note: This sequence is shown  
 CC in this orientation (5' to 3') in the disclosure of the specification.  
 CC but is shown in the opposite orientation in the sequence listing  
 XX  
 SEQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 QY  
 Query Match 2.0%; Score 12; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 16 ATGACCGGAGG 27  
 18 ATGACCGGAGG 7  
 XX  
 RESULT 212  
 AAL51414  
 ID AAL51414 standard; DNA; 18 BP.  
 XX  
 AC AAL51414;  
 XX  
 DT 27-MAR-2003 (first entry)  
 DE Probe carrier manufacturing method-related oligonucleotide, SEQ ID NO. 1.  
 XX  
 KM Probe; ss; probe carrier manufacture; DNA micro-chips.  
 XX  
 OS Unidentified.  
 XX  
 PN JP200257836-A.  
 XX  
 PD 11-SEP-2002.  
 XX  
 PF 28-FEB-2001; 2001JP-00055971.  
 XX  
 PR 28-FEB-2001; 2001JP-00055971.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2003-106341/10.  
 XX  
 PT Manufacturing a probe carrier used for analyzing a base sequence of  
 PT genetic DNA, comprises discharging a probe solution in a cavity located  
 PT at each probe position on a probe carrier through a group of discharging  
 PT openings.  
 XX  
 PS Example 4; Page 12; 18pp; Japanese.  
 XX  
 CC The invention comprises a method for manufacturing a probe carrier. The  
 CC method involves discharging and fixing probe solutions in the  
 CC corresponding cavities according to information on the positions of  
 CC respective types of probes. The method of the invention is useful for  
 CC manufacturing probe carriers (e.g. DNA micro-chips). The present DNA

CC sequence represents an oligonucleotide used in the method of the  
 CC invention  
 XX  
 SEQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 QY  
 Query Match 2.0%; Score 12; DB 7; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 16 ATGACCGGAGG 27  
 1 ATGACCGGAGG 12  
 XX  
 RESULT 213  
 ADC54006  
 ID ADC54006 standard; DNA; 18 BP.  
 XX  
 AC ADC54006;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE Oligonucleotide of the invention SEQ ID NO:1.  
 XX  
 KM ss; probe carrier; discharge.  
 XX  
 OS Synthetic.  
 XX  
 PN JP2003035711-A.  
 XX  
 PD 07-FEB-2003.  
 XX  
 PF 28-MAR-2002; 2002JP-00093023.  
 XX  
 PR 28-MAR-2001; 2001JP-00094400.  
 XX  
 PA (CANO ) CANON KK.  
 XX  
 DR WPI; 2003-535999/51.  
 XX  
 PT Probe carrier manufacturing method for inkjet system, involves scanning  
 PT liquid discharge head in direction orthogonal to scanning direction, at  
 PT angle satisfying predetermined relation.  
 XX  
 PS Example 2; SEQ ID NO. 1; 17pp; Japanese.  
 XX  
 CC The invention relates to a novel probe carrier and the method for  
 CC manufacturing the carrier. The invention enables stable discharge of  
 CC solution, and removes liquid droplets adhering to discharge nozzle. The  
 CC present sequence is used in the exemplification of the invention.  
 XX  
 SEQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;  
 QY  
 Query Match 2.0%; Score 12; DB 9; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 16 ATGACCGGAGG 27  
 1 ATGACCGGAGG 12  
 XX  
 RESULT 214  
 ADC54007/C  
 ID ADC54007 standard; DNA; 18 BP.  
 XX  
 AC ADC54007;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DE Oligonucleotide of the invention SEQ ID NO:2.  
 XX  
 KM ss; probe carrier; discharge.

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XX OS Synthetic.
XX PN JP2003035711-A.
XX PD 07-FEB-2003.
XX PF 28-MAR-2002; 2002JP-00093023.
XX PR 28-MAR-2001; 2001JP-00094400.
XX PA (CANO ) CANON KK.
XX DR WPI; 2003-S35999/51.
XX PT Probe carrier manufacturing method for inkjet system, involves scanning
XX PT liquid discharge head in direction orthogonal to scanning direction, at
XX PT angle satisfying predetermined relation.
XX PS Example 2; SEQ ID NO 2; 17bp; Japanese.
XX CC The invention relates to a novel probe carrier and the method for
XX CC manufacturing the carrier. The invention enables stable discharge of
XX CC solution, and removes liquid droplets adhering to discharge nozzle. The
XX CC present sequence is used in the exemplification of the invention.
XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGAACCGAGG 27
   |||||
Db 18 ATGAACCGAGG 7

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RESULT 215
AAT43666
ID AAT43666 standard; DNA; 19 BP.
XX
XX AAT43666;

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DT 19-AUG-1997 (first entry)
XX

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DE HIV-1 matrix protein p17 gene probe 3.
XX

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```

KW Human immunodeficiency virus type 1; subtype B; transmissible;
KW matrix protein p17; prognosis; probe; detection; maternal transmission;
KW hybridisation assay; immunoassay; ss.
XX

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OS Synthetic.
XX

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PN EP743364-A2.
XX

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PD 20-NOV-1996.
XX

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PF 17-MAY-1996; 96EP-00401084.
XX

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PR 18-MAY-1995; 95FR-00005914.
XX

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PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX

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PI Narwa R, Roques P;
XX

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DR WPI; 1996-507733/51.
XX

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PT Human immunodeficiency virus p17 gene fragments, derived proteins and
PT antibodies - useful for assessing the risk of maternal transmission of
PT HIV-1 infection.
XX

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PS Claim 15; Page 29; 46pp; French.
XX

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CC A set of six oligonucleotide probes enable the risk of maternal- foetal
CC transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
CC AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
CC transmitted to the foetus; probes 2-4 (see AAT43665-T43668) allow
CC detection of strains which are never transmitted from mother to foetus.
CC The present sequence is that of probe 3 and it detects PAL, HMI, AWO,
CC CHER, GOR, MOE, SIM, FLO, 2759, 2826, 4501, 4538 and 5613 HIV-1 sequences
XX
XX SQ Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
   |||||
Db 4 TTGCTCTTCCTC 15

```

```

RESULT 216
AAT43665
ID AAT43665 standard; DNA; 19 BP.
XX
XX AAT43665;

```

```

DT 19-AUG-1997 (first entry)
XX

```

```

DE HIV-1 matrix protein p17 gene probe 2.
XX

```

```

KW Human immunodeficiency virus type 1; subtype B; transmissible;
KW matrix protein p17; prognosis; probe; detection; maternal transmission;
KW hybridisation assay; immunoassay; ss.
XX

```

```

OS Synthetic.
XX

```

```

PN EP743364-A2.
XX

```

```

PD 20-NOV-1996.
XX

```

```

PF 17-MAY-1996; 96EP-00401084.
XX

```

```

PR 18-MAY-1995; 95FR-00005914.
XX

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PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX

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PI Narwa R, Roques P;
XX

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DR WPI; 1996-507733/51.
XX

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PT Human immunodeficiency virus p17 gene fragments, derived proteins and
PT antibodies - useful for assessing the risk of maternal transmission of
PT HIV-1 infection.
XX

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PS Claim 15; Page 29; 46pp; French.
XX

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```

CC A set of six oligonucleotide probes enable the risk of maternal- foetal
CC transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
CC AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
CC transmitted to the foetus; probes 2-4 (see AAT43665-T43668) allow
CC detection of strains which are never transmitted from mother to foetus.
CC The present sequence is that of probe 2 and it detects HAR, LOUB, VIL and
CC 2754 HIV-1 sequences
XX

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```

SQ Sequence 19 BP; 1 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

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Query Match          2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
   |||||
Db 4 TTGCTCTTCCTC 15

```

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RESULT 217
PD AAT43667
ID AAT43667 standard; DNA; 19 BP.
XX
XX
AC AAT43667;
XX
XX 19-AUG-1997 (first entry)
DT
XX
XX HIV-1 matrix protein p17 gene probe 4.
DE
XX
XX Human immunodeficiency virus type 1; subtype B; transmissible;
KM matrix protein p17; prognosis; probe; detection; maternal transmission;
KM hybridisation assay; immunassay; ss.
XX
XX Synthetic.
XX
XX EP743364-A2.
PN
XX 20-NOV-1996.
PD
XX
XX 17-MAY-1996; 96EP-00401084.
PF
XX
XX 18-MAY-1995; 95PR-00005914.
PR
XX
XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
PA
XX
XX Narwa R, Roques P;
PI
XX
XX WPI; 1996-507733/51.
DR
XX
XX Human immunodeficiency virus p17 gene fragments, derived proteins and
PT antibodies - useful for assessing the risk of maternal transmission of
PT HIV-1 infection.
XX
XX Claim 15; Page 29; 46pp; French.
PS
XX
XX A set of six oligonucleotide probes enable the risk of maternal- foetal
CC transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
CC AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
CC transmitted to the foetus; probes 2-4 (see AAT43665-743668) allow
CC detection of strains which are never transmitted from mother to foetus.
CC The present sequence is that of probe 4 and it detects the CEL HIV-1
CC sequence
XX
XX Sequence 19 BP; 1 A; 7 C; 2 G; 9 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
DB 3 TTGCTCTTCCTC 14

```

```

XX
XX 22-MAY-1997.
PD
XX
XX 13-NOV-1996; 96WO-US018273.
PF
XX
XX 14-NOV-1995; 95US-0006692P.
PR
XX
XX (MINTU ) UNIV MINNESOTA.
PA
XX
XX Verfallle CM, McIvor RS, Zhao RC;
PI
XX
XX WPI; 1997-289281/26.
DR
XX
XX Expression cassette for forming drug resistant hematopoietic stem cells -
PT decreases RNA or protein found only in malignant cells; for treating
PT leukaemia(s), such as chronic myelogenous leukaemia.
XX
XX
XX Example 2; Fig 1; 52pp; English.
PS
XX
XX This beta-actin 5' RT-PCR primer is used in a novel method of preparing
CC drug-resistant, non-malignant haematopoietic cells. This method involves
CC the construction of a new expression cassette comprising a first nucleic
CC acid molecule which encodes resistance of a host cell to a cytotoxic
CC agent, operably linked to a first promoter which functions in the host
CC cell and a second nucleic acid molecule operably linked to a second
CC promoter which functions in the host cell. The second nucleic acid
CC molecule encodes an RNA molecule or a polypeptide whose expression
CC decreases the expression of an RNA or a polypeptide present in a
CC malignant cell only. This method can eliminate residual neoplastic
CC disease in a patient, where the disease has an immature hematopoietic
CC progenitor cell with a well-defined gene rearrangement. Diseases such as
CC chronic myelogenous leukemia which is associated with a BCR/ABL gene
CC rearrangement, acute lymphoblastic leukaemia and acute promyelocytic
CC leukaemia may be treated using this method
XX
XX
XX Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 TGAGATCTTCA 328
DB 19 TGAGATCTTCA 8

```

```

RESULT 218
AAT68898/c
ID AAT68898 standard; DNA; 19 BP.
XX
XX AAT68898;
AC
XX
XX 06-APR-1998 (first entry)
DT
XX
XX Human beta-actin 5' RT-PCR primer.
DE
XX
XX Drug-resistance; neoplastic disease; non-malignant haematopoietic cell;
KM progenitor; gene rearrangement; RT-PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
PA
XX
XX WO9718305-A2.
PN

```

```

RESULT 219
AAT68899/c
ID AAT68899 standard; DNA; 19 BP.
XX
XX AAT68899;
AC
XX
XX 06-APR-1998 (first entry)
DT
XX
XX Human beta-actin 3' RT-PCR primer.
DE
XX
XX Drug-resistance; neoplastic disease; non-malignant haematopoietic cell;
KM progenitor; gene rearrangement; RT-PCR primer; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
XX
XX WO9718305-A2.
PN
XX
XX 22-MAY-1997.
PD
XX
XX 13-NOV-1996; 96WO-US018273.
PF
XX
XX 14-NOV-1995; 95US-0006692P.
PR
XX
XX (MINTU ) UNIV MINNESOTA.
PA
XX
XX Verfallle CM, McIvor RS, Zhao RC;
PI

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XX
DR WPI; 1997-269281/26.
XX
PT Expression cassette for forming drug resistant hematopoietic stem cells -
PT decreases RNA or protein found only in malignant cells; for treating
PT leukaemia(s), such as chronic myelogenous leukaemia.
XX
PS Example 2; Fig 1; 52pp; English.
XX
CC This beta-actin 3' RT-PCR primer is used in a novel method of preparing
CC drug-resistant, non-malignant hematopoietic cells. This method involves
CC the construction of a new expression cassette comprising a first nucleic
CC acid molecule which encodes resistance of a host cell to a cytotoxic
CC agent, operably linked to a first promoter which functions in the host
CC cell and a second nucleic acid molecule operably linked to a second
CC promoter which functions in the host cell. The second nucleic acid
CC molecule encodes an RNA molecule or a polypeptide whose expression
CC decreases the expression of an RNA or a polypeptide present in a
CC malignant cell only. This method can eliminate residual neoplastic
CC disease in a patient, where the disease has an immature hematopoietic
CC progenitor cell with a well-defined gene rearrangement. Diseases such as
CC chronic myelogenous leukaemia which is associated with a BCR/ABL gene
CC rearrangement acute lymphoblastic leukaemia and acute promyelocytic
CC leukaemia may be treated using this method
XX
SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 317 TGAGGATCTTCA 328
19 TGAGGATCTTCA 8
DB
RESULT 220
AAV40952/C
ID AAV40952 standard; DNA; 19 BP.
XX
AC AAV40952;
XX
DT 25-SEP-1998 (first entry)
XX
DE Primer BCRA1B;1698U9 for abnormality detection.
XX
KM PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
KM lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
KM medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824928-A2.
XX
PD 11-JUN-1998.
XX
PF 08-DEC-1997; 97WO-DK000556.
XX
PR 06-DEC-1996; 96DK-00001401.
XX
PA (PALU/) PALISGAARD N.
PI Pallsgaard N; Hokland P;
XX
DR WPI; 1998-333344/29.
XX
PT Detection of chromosomal abnormalities - by subjecting patient sample
PT nucleic acids to a multiplex molecular amplification procedure using
PT primers specific for characteristic nucleic acid sequence.
PS Claim 73; Page 74; 126pp; English.
XX

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```

CC This sequence represents a primer used in the method of the invention for
CC the detection of the presence or absence of chromosomal abnormalities,
CC each abnormality being associated with a condition in a subject and each
CC being defined by at least one characteristic nucleic acid sequence. The
CC method comprises: (a) obtaining a sample of nucleic acids derived from a
CC subject which may harbour one of the chromosomal abnormalities; (b)
CC subjecting the sample to a multiplex molecular amplification (MMA)
CC procedure, where a number of the characteristic sequences, if present in
CC a sufficient amount, will be amplified; (c) retrieving the product(s)
CC from step (b), and detecting the presence and/or absence of an amplicon
CC characteristic of the abnormal sequences to detect the presence or
CC absence of corresponding chromosomal abnormalities; where the MMA
CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
CC in one single reaction mixture, each of the primers defining an end of at
CC least one characteristic nucleic acid sequence, and where at least one of
CC the primers defines the first end of at least two characteristic nucleic
CC acid sequences, the characteristic nucleic acid sequences each being
CC determined in their opposite ends by MDP selected from the remainder of
CC the MDP. The methods can be used for detecting chromosomal abnormalities
CC associated with diseases including numerous leukaemia's, lymphoma's,
CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX
SQ Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 290 TTCTGCAGGGA 301
17 TTCTGCAGGGA 6
DB
RESULT 221
AAA13623
ID AAA13623 standard; DNA; 19 BP.
XX
AC AAA13623;
XX
DT 20-JUL-2000 (first entry)
XX
DE Human oncofoetal ferritin 1 PCR primer #8.
XX
KM Human; oncofoetal ferritin 1; OFP1; ferritin; transplation;
KM pathological pregnancy; breast cancer; cytostatic; immunosuppressive;
KM contraceptive; abortive; neotrophic; vaccine; immunisation; cancer;
KM transplant rejection; autoimmune disease; fertilisation; diagnosis;
KM in vitro fertilization; IVF; heptablastoma; Hodgkin's lymphoma;
KM leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;
KM spontaneous abortion; miscarriage; premature contraction; toxemia;
KM premature delivery; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200015788-A2.
XX
PD 23-MAR-2000.
XX
PF 08-SEP-1999; 99WO-IL000485.
XX
PR 11-SEP-1998; 98IL-00126181.
XX
PA (GARD-) GARDINO INVESTMENT NV.
PI Moroz C;
XX
DR WPI; 2000-271427/23.
XX
PT DNA sequence coding for oncofoetal ferritin 1 protein, useful for
PT immunizations against breast cancer, for enhancing fertilization rates
PT during in vitro fertilization treatment and for use as a growth factor of
PT bone-marrow progenitor cells.
XX

```

XX Claim 23; Page 49; 66pp; English.

XX The present sequence represents a specifically claimed PCR primer used in

CC the isolation of oncofetal ferritin 1 (OFPI) protein. OFPI has

CC cytotactic, immunosuppressive, contraceptive, abortive and neutrotic

CC activities, and can be used as a vaccine. Compositions comprising the

CC expression vector containing an OFPI coding sequence, and the OFPI

CC protein, are useful: (a) for immunisations against cancer, especially

CC breast cancer; (b) in the treatment of transplant rejection, autoimmune

CC diseases, pathological pregnancies; (c) for enhancing fertilisation rates

CC during in vitro fertilisation (IVF) treatment; and (d) for use as a

CC growth factor of bone-marrow progenitor cells such as granulocyte

CC monocytes. The OFPI nucleotide sequence is useful for diagnosing cancer

CC such as breast cancer, hepatoblastoma, leukaemia, Hodgkin's and non-

CC Hodgkin's lymphomas and embryonal tumours, Down's Syndrome, and

CC pathological pregnancies such as spontaneous abortion and miscarriage,

CC premature contractions, toxemia or premature delivery

XX Sequence 19 BP; 3 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 3; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGCCCC 257

DB 7 CTCCTGAGCCCC 18

RESULT 222

AAZ76946/c

ID AAZ76946 standard; DNA; 19 BP.

XX AC AAZ76946;

XX 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:11302.

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation;

XX amplification; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX Homo sapiens.

XX WO954500-A2.

XX 28-OCT-1999.

XX 21-APR-1999; 95MO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX Claim 9; Page 2640; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC nucleotide, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

XX present invention

XX Sequence 19 BP; 9 A; 1 C; 9 G; 0 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 3; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTCC 187

DB 15 TGCTCTTCCTCC 4

RESULT 223

AAC70391

ID AAC70391 standard; DNA; 19 BP.

XX AC AAC70391;

XX 09-FEB-2001 (first entry)

XX Single nucleotide polymorphism PCR primer #148.

XX Single nucleotide polymorphism; SNP; human; genetic disease;

XX disease susceptibility; cardiovascular system; endocrine system;

XX neurological system; forensic testing; paternity testing; PCR primer; ss.

XX Homo sapiens.

XX WO200058519-A2.

XX 05-OCT-2000.

XX 30-MAR-2000; 2000MO-US008440.

XX 31-MAR-1999; 99US-0127248P.

XX (WHD) WHITEHEAD INST BIOMEDICAL RES.

XX (AFY-) AFFYMETRIX INC.

XX Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;

PI Lipshutz RJ, Petzl N, Sklar P;

XX WPI; 2000-611722/58.

XX Nucleic acid selected from one of 106 genes comprising single nucleotide

PT polymorphisms, allele-specific oligonucleotides to the genes are useful

PT for phenotypic correlations, forensics, paternity testing, medicine and

PT genetic analysis.

XX Claim 8; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single

CC nucleotide polymorphisms (SNPs) which the inventors identified in human

CC genes. These SNPs can be used in disease diagnosis and prediction of an

CC individual's susceptibility to disease, in forensic and paternity testing

CC and in genetic mapping. In particular, the SNPs of the invention can be

CC used to diagnose susceptibility to diseases of the cardiovascular,

CC endocrine and neurological systems, such as coronary artery disease,

CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's

CC diseases

XX Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;



PN WO200168853-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 14-MAR-2001; 2001WO-US007896.  
 XX  
 PR 14-MAR-2000; 2000US-0189226P.  
 PR 28-DEC-2000; 2000US-0258452P.  
 XX  
 PA (UYUO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
 XX  
 PI Roden R, Naora H;  
 XX  
 DR WPI; 2001-596909/67.  
 XX  
 PT Novel cancer-related antigen useful for prognosis, diagnosis and  
 PT treatment of cancer, especially ovarian cancer in an individual,  
 PT comprises a fragment isolated from bacteriophage lambda.  
 PS  
 PS Example 5; Page 40; 67pp; English.  
 XX  
 CC The patent discloses autoantibodies in cancer patients specific for novel  
 CC cancer-related antigens that are normally intracellular including  
 CC homeobox proteins, HoxA7, HoxB7, ADP ribosylation factor 1 (Arf-1), ATP  
 CC dependent iron transporter ABC-7 and a novel protein encoded by  
 CC BCOR1/Xho1 fragment isolated from bacteriophage lambda clone 44B.1. The  
 CC presence of these autoantibodies is correlated with neoplastic processes  
 CC in patients. Proteins of the invention are useful for screening for  
 CC cancer in an individual. HoxB7 is useful for screening for cancer other  
 CC than breast cancer, renal cell carcinoma, colon cancer or melanoma in an  
 CC individual, by determining whether cells in the individual are expressing  
 CC a gene product of HoxB7, expression of which is correlated with increased  
 CC likelihood of cancer in the individual. It is useful for screening  
 CC ovarian cancer or benign serous cystadenoma. HoxB7 proteins are useful to  
 CC distinguish between neoplastic and non-neoplastic fluid accumulations in  
 CC patients carrying a malignant diagnosis and in screening methods for  
 CC therapeutically active materials. HoxB7 antibodies are useful for  
 CC detecting epitopes found on proteins of the invention in histological  
 CC sections of ovarian cancer tissue as well as in other solid tumours such  
 CC as breast cancer and melanoma. The proteins of the invention are also  
 CC used as vaccines. The present DNA sequence is a PCR primer which is used  
 CC for amplifying human beta-actin DNA  
 XX  
 SQ Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 317 TGAAGATCTTCA 328  
 |||||  
 DB 8 TGAAGATCTTCA 19

PF 01-MAR-2000; 2000GB-00005005.  
 XX  
 PR 01-MAR-2000; 2000GB-00005005.  
 XX  
 PA (NOVS ) NOVARTIS RES FOUND.  
 XX  
 PI Dumas F, Van Gelder P, Duckely M, Hohn B;  
 XX  
 DR WPI; 2001-618844/72.  
 XX  
 PT Delivering a material across a membrane, useful for producing transiently  
 PT or stably transfected or transformed cells, comprises introducing  
 PT Agrobacterium VirE2 into a membrane, where VirE2 forms a channel through  
 PT the membrane.  
 XX  
 PS Example 1; Page 21; 30pp; English.  
 XX  
 CC The invention relates to a method of delivering a material across a  
 CC membrane. The method involves introducing Agrobacterium VirE2, its  
 CC fragment or homologue into a membrane, where VirE2, its fragment or  
 CC homologue forms a channel through the membrane; contacting the membrane  
 CC with a molecule desired to be transferred across the membrane; and  
 CC allowing the molecule to cross the membrane through the channel. The  
 CC method is useful in delivering materials across membranes, particularly  
 CC into cells or organelles, and subsequently producing transiently or  
 CC stably transfected or transformed cells. The method is especially useful  
 CC for delivering nucleic acid to a cell to achieve expression of a desired  
 CC transgene by the cell, and for treating cancer cells, relying on a new  
 CC non-viral system without ITR and the possible hazards connected with  
 CC them. The present sequence represents a VirE2 specific oligo used in the  
 CC method of the invention  
 XX  
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;  
 XX  
 Query Match 2.0%; Score 12; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 TTGATGACCGG 24  
 |||||  
 DB 3 TTGATGACCGG 14

RESULT 227  
 ABL58227  
 ID ABL58227 standard; DNA; 19 BP.  
 XX  
 AC ABL58227;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE A. tumefaciens VirE2 DNA specific oligonucleotide.  
 XX  
 KM VirE2; cytostatic; gene therapy; transfection; transformation;  
 KM virulence protein; ss.  
 OS  
 OS Agrobacterium tumefaciens.  
 XX  
 XX GB2359812-A.  
 XX  
 PD 05-SEP-2001.  
 XX

RESULT 228  
 AAF84826  
 ID AAF84826 standard; cDNA; 19 BP.  
 XX  
 AC AAF84826;  
 XX  
 DT 09-JUL-2001 (first entry)  
 XX  
 DE PCR primer used for RACE-PCR reactions of human SPG4 cDNA.  
 XX  
 KM Human; SPG4 gene; spactin; PSF-AD; gene therapy; probe;  
 KM autosomal dominant familial spastic paraplegia; PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX FR2798138-A1.  
 XX  
 PD 09-MAR-2001.  
 XX  
 PF 03-SEP-1999; 99FR-00011097.  
 XX  
 PR 03-SEP-1999; 99FR-00011097.  
 PR (CNRS ) CNRS CENT NAT RECH SCI.  
 PA  
 PI Weissenbach J, Hazan J;  
 XX  
 XX WPI; 2001-283966/30.  
 DR  
 XX New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of

PT autosomal dominant familial spastic paraplegia and in drug screening.  
XX  
PS Claim 5; Page 24; 145pp; French.  
XX  
CC PCR primers ABK89543-27 were used in RACE-PCR reactions of human SPG4  
CC gene cDNA. The primers may also be used as probes. The SPG4 gene encodes  
CC a spastin polypeptide. Mutations in the SPG4 gene are responsible for  
CC autosomal dominant familial spastic paraplegia. SPG4 polynucleotides, and  
CC their fragments, are used to screen DNA banks for sequences that encode  
CC spastin (particularly sequences in other mammals, specifically mice); to  
CC identify SPG4 mutations, or other genetic anomalies, particularly for  
CC diagnosis of autosomal dominant familial spastic paraplegia (PSF-AD); to  
CC identify promoters and other regulatory elements of the SPG4 gene; for  
CC detection and amplification; for recombinant production of spastin; and  
CC for diagnostic genotyping of PSF-AD  
XX  
SQ Sequence 19 BP; 4 A; 5 C; 3 G; 7 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 12; DB 5; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 441 CTGGAATACTTT 452  
1 CTGGAATACTTT 12  
XX  
RESULT 229  
ABK89543/c  
ID ABK89543 standard; DNA; 19 BP.  
XX  
AC ABK89543;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Synthetic PCR primer Acctf.  
XX  
KM Barley yellow dwarf virus infection; BYDV; plant resistance;  
KM monocotyledon; wheat; Triticum; Sorghum; rice; Oryza; barley; Hordeum;  
KM maize; Zea; Tye; Secale; triticales; oat; Avena; antiviral; gene therapy;  
KM PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN WO200248394-A1.  
XX  
PD 20-JUN-2002.  
XX  
PF 13-DEC-2001; 2001WO-AU001611.  
XX  
PR 15-DEC-2000; 2000AU-00002103.  
XX  
PR 21-MAY-2001; 2001US-0292778P.  
XX  
PA (GRAI-) GRAIN BIOTECHNOLOGY AUSTRALIA PTY LTD.  
XX  
PI Bower R, Lehto K, Junttila TT, Yang R, Pehu E;  
XX  
PI WPI; 2002-56353/62.  
XX  
PT Protecting plant from barley yellow dwarf virus infection, by  
PT transforming modified nucleic acid expressing translationally-altered RNA  
PT into a plant cell, which confers resistance against virus infection.  
XX  
PS Example 9; Page 60; 89pp; English.  
XX  
CC The present invention relates to a new method of protecting a plant from  
CC barley yellow dwarf virus (BYDV) infection. The method of the invention  
CC comprises transforming a modified nucleic acid molecule into a plant  
CC cell, where the expression of the nucleic acid molecule results in the  
CC expression of a translationally-altered RNA molecule which confers to the  
CC plant resistance against infection with BYDV. The method is useful for  
CC protecting a plant from BYDV infection, where the plant is a  
CC monocotyledon selected from wheat (Triticum), sorghum (Sorghum), rice

CC (Oryza), barley (Hordeum), maize (Zea), rye (Secale), triticales and oat  
CC (Avena), preferably wheat. The present nucleic acid sequence represents a  
CC synthetic PCR primer that was used in the methods of the invention  
XX  
SQ Sequence 19 BP; 6 A; 6 C; 3 G; 4 T; 0 U; 0 Other;  
XX  
Query Match 2.0%; Score 12; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
QY 317 TGAGATCTTCA 328  
18 TGAGATCTTCA 7  
XX  
DB  
XX  
RESULT 230  
ADA03189  
ID ADA03189 standard; DNA; 19 BP.  
XX  
AC ADA03189;  
XX  
DT 06-NOV-2003 (first entry)  
XX  
DE Wild type sequence in human p53 around position R249S in mutant gene.  
XX  
KM cytosolic; virucide; anti-HIV; neuroprotective; ophthalmological;  
KM antidiabetic; antispasmodic; antineumatic; antiarthritic; ds;  
KM inhibitor repression; inhibitor RNA; apoptosis; necrosis;  
KM differentiation; tumour cell division; BCL2 gene family;  
KM matrix metalloproteinase; membrane metalloproteinase;  
KM nuclear hormone receptor; transcription factor;  
KM vascular endothelial growth factor; p53; chromosomal translocation;  
KM leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;  
KM AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;  
KM psoriasis; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040366-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 08-NOV-2002; 2002WO-FR003843.  
XX  
PR 09-NOV-2001; 2001FR-00014549.  
XX  
PR 10-APR-2002; 2002FR-00004474.  
XX  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
XX  
PI Harel-Bellan A, Alt-St-Al S, Cabon-Georget F, Chauchereau A;  
PI Dautry F;  
XX  
XX WPI; 2003-441571/41.  
XX  
PT New double-stranded oligonucleotides, useful e.g. for treatment and  
PT diagnosis of tumors, comprise complementary strands with single-stranded  
PT overhangs.  
XX  
PS Disclosure; Page 17; 148pp; French.  
XX  
CC The invention relates to double-stranded oligonucleotides consisting of  
CC two complementary strands (1a; 1b), each having 1-5 unpaired nucleotides,  
CC at either at their 3' and 5' ends, forming single-stranded overhangs. One  
CC of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),  
CC that is to be specifically repressed. The oligonucleotides are preferably  
CC double stranded inhibitor RNA molecules with a couple of thymidine bases  
CC attached at the 3' or 5' ends. The targets are preferably nucleic acids  
CC that, when repressed, induce apoptosis, necrosis or differentiation of  
CC tumour cells and/or inhibit division of such cells. Typical of many  
CC specified targets include: genes of the BCL2 family; genes that encode  
CC metalloproteinases (matrix or membrane) or their inhibitors; genes encoding  
CC mutant forms of nuclear hormone receptors; a sequence encoding the Hfl-  
CC alpha transcription factor; sequences encoding various isoforms of the

CC vascular endothelial growth factor; viral genes; genes that express a  
 CC mutated protein, e.g. inactive p53; genes that are formed by a  
 CC chromosomal translocation, e.g. where associated with leukaemia, and  
 CC genes that express androgen receptors. The oligonucleotides are used: (i)  
 CC to study gene function; (ii) for therapy or diagnosis, particularly of  
 CC conditions caused by expression of a harmful gene or fusion protein.  
 CC specifically cancer (e.g. associated with expression of mutant p53 or of  
 CC the human papilloma virus B6 protein), viral infections, especially AIDS  
 CC or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD  
 CC / and (iii) for treating hypervascular diseases, e.g. age-related macular  
 CC degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis  
 CC and rheumatoid arthritis. They may also be used in vitro, e.g. for  
 CC treating transplants and for establishing a genetic profile, for  
 CC individualization, or modification, of treatment regimes. They provide  
 CC very effective and very specific repression of genes. RNA hybrids are  
 CC more stable than either hybrids prepared from DNA or single-stranded  
 CC sequences; contain only natural components (so will not induce  
 CC immunological or intolerance reactions) and they enter tumour cells more  
 CC effectively than plasmids. This sequence represents the sequence in the  
 CC wild type human p53 gene around the position of mutation R248S. The  
 CC oligonucleotides of the invention can be targeted to this sequence.

XX  
 SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ATGACC GGAGG 27  
 |||||  
 Db 3 ATGACC GGAGG 14

RESULT 231  
 ADA03188  
 XX ADA03188 standard; DNA; 19 BP.  
 AC ADA03188;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX

DE Wild type sequence in human p53 around position R248W in mutant gene.  
 XX  
 XX cytostatic; virocidic; anti-HIV; neuroprotective; ophthalmological;  
 XX antidiabetic; antipsoriatic; antirheumatic; antiarthritic; de;  
 XX inhibitor repression; inhibitor RNA; apoptosis; necrosis;  
 XX differentiation; tumour cell division; BCL2 gene family;  
 XX matrix metalloprotease; membrane metalloprotease;  
 XX nuclear hormone receptor; transcription factor;  
 XX vascular endothelial growth factor; p53; chromosomal translocation;  
 XX leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;  
 XX AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;  
 XX psoriasis; rheumatoid arthritis.

XX  
 OS Homo sapiens.  
 XX  
 PN MO2003040366-A2.  
 XX  
 PD 15-MAY-2003.  
 XX  
 PF 08-NOV-2002; 2002WO-FR003843.  
 XX  
 PR 09-NOV-2001; 2001FR-00014549.  
 XX  
 PR 10-APR-2002; 2002FR-00004474.  
 XX  
 PA (CNRS) CNRS CENT NAT RECH SCI.  
 XX  
 PI Harel-Bellan A, Alt-St-Ali S, Cabon-Georget F, Chachereau A;  
 XX Dautry F;  
 DR WPI, 2003-441571/41.  
 XX  
 PT New double-stranded oligonucleotides, useful e.g. for treatment and

PT diagnosis of tumours, comprise complementary strands with single-stranded  
 PT overhangs.

XX  
 XX Disclosure; Page 17; 148pp; French.

PS  
 CC The invention relates to double-stranded oligonucleotides consisting of  
 CC two complementary strands (1a, 1b), each having 1-5 unpaired nucleotides,  
 CC at either at their 3' and 5' ends, forming single-stranded overhangs. One  
 CC of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),  
 CC that is to be specifically repressed. The oligonucleotides are preferably  
 CC double stranded inhibitor RNA molecules with a couple of thymidine bases  
 CC attached at the 3' or 5' ends. The targets are preferably nucleic acids  
 CC that, when repressed, induce apoptosis, necrosis or differentiation of  
 CC tumour cells and/or inhibit division of such cells. Typical of many  
 CC specified targets include: genes of the BCL2 family; genes that encode  
 CC metalloproteases (matrix or membrane) or their inhibitors; genes encoding  
 CC mutant forms of nuclear hormone receptors; a sequence encoding the Hfl-  
 CC alpha transcription factor; sequences encoding various isoforms of the  
 CC vascular endothelial growth factor; viral genes; genes that express a  
 CC mutated protein, e.g. inactive p53; genes that are formed by a  
 CC chromosomal translocation, e.g. where associated with leukaemia, and  
 CC genes that express androgen receptors. The oligonucleotides are used: (i)  
 CC to study gene function; (ii) for therapy or diagnosis, particularly of  
 CC conditions caused by expression of a harmful gene or fusion protein,  
 CC specifically cancer (e.g. associated with expression of mutant p53 or of  
 CC the human papilloma virus B6 protein), viral infections, especially AIDS  
 CC or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD  
 CC / and (iii) for treating hypervascular diseases, e.g. age-related macular  
 CC degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis  
 CC and rheumatoid arthritis. They may also be used in vitro, e.g. for  
 CC treating transplants and for establishing a genetic profile, for  
 CC individualization, or modification, of treatment regimes. They provide  
 CC very effective and very specific repression of genes. RNA hybrids are  
 CC more stable than either hybrids prepared from DNA or single-stranded  
 CC sequences; contain only natural components (so will not induce  
 CC immunological or intolerance reactions) and they enter tumour cells more  
 CC effectively than plasmids. This sequence represents the sequence in the  
 CC wild type human p53 gene around the position of mutation R248W. The  
 CC oligonucleotides of the invention can be targeted to this sequence.

XX  
 SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ATGACC GGAGG 27  
 |||||  
 Db 3 ATGACC GGAGG 14

RESULT 232  
 ADA03187  
 XX ADA03187 standard; DNA; 19 BP.  
 AC ADA03187;  
 XX  
 DT 06-NOV-2003 (first entry)  
 XX

DE Wild type sequence in human p53 around position R248Q in mutant gene.  
 XX  
 XX cytostatic; virocidic; anti-HIV; neuroprotective; ophthalmological;  
 XX antidiabetic; antipsoriatic; antirheumatic; antiarthritic; de;  
 XX inhibitor repression; inhibitor RNA; apoptosis; necrosis;  
 XX differentiation; tumour cell division; BCL2 gene family;  
 XX matrix metalloprotease; membrane metalloprotease;  
 XX nuclear hormone receptor; transcription factor;  
 XX vascular endothelial growth factor; p53; chromosomal translocation;  
 XX leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;  
 XX AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;  
 XX psoriasis; rheumatoid arthritis.

XX  
 OS Homo sapiens.

XX WO2003040366-A2.  
 XX 15-MAY-2003.  
 XX 08-NOV-2002; 2002WO-FR003843.  
 XX 09-NOV-2001; 2001FR-00014549.  
 XX 10-APR-2002; 2002FR-00004474.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Harel-Bellan A, Ait-Si-All S, Cabon-Georget F, Chauchereau A;  
 XX Dauray F;  
 XX WPI; 2003-441571/41.  
 XX New double-stranded oligonucleotides, useful e.g. for treatment and  
 XX diagnosis of tumors, comprise complementary strands with single-stranded  
 XX overhangs.  
 XX Disclosure; Page 17; 148pp; French.  
 XX The invention relates to double-stranded oligonucleotides consisting of  
 XX two complementary strands (Ia; Ib), each having 1-5 unpaired nucleotides,  
 XX at either at their 3' and 5' ends, forming single-stranded overhangs. One  
 XX of (Ia) and (Ib) is complementary to a target sequence, (DNA or RNA),  
 XX that is to be specifically repressed. The oligonucleotides are preferably  
 XX double stranded inhibitor RNA molecules with a couple of thymidine bases  
 XX attached at the 3' or 5' ends. The targets are preferably nucleic acids  
 XX that, when repressed, induce apoptosis, necrosis or differentiation of  
 XX tumour cells and/or inhibit division of such cells. Typical of many  
 XX specified targets include: genes of the BCL2 family; genes that encode  
 XX metalloproteases (matrix or membrane) or their inhibitors; genes encoding  
 XX mutant forms of nuclear hormone receptors; a sequence encoding the Hfl-  
 XX alpha transcription factor; sequences encoding various isoforms of the  
 XX vascular endothelial growth factor; viral genes; genes that express a  
 XX mutated protein, e.g. inactive p53; genes that are formed by a  
 XX chromosomal translocation, e.g. where associated with leukemia, and  
 XX genes that express androgen receptors. The oligonucleotides are used: (1)  
 XX to study gene function; (ii) for therapy or diagnosis, particularly of  
 XX conditions caused by expression of a harmful gene or fusion protein,  
 XX specifically cancer (e.g. associated with expression of mutant p53 or of  
 XX the human papilloma virus E6 protein), viral infections, especially AIDS  
 XX or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD  
 XX ; and (iii) for treating hypervascular diseases, e.g. age-related macular  
 XX degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis  
 XX and rheumatoid arthritis. They may also be used in vitro, e.g. for  
 XX treating transplants and for establishing a genetic profile, for  
 XX individualization, or modification, of treatment regimes. They provide  
 XX very effective and very specific repression of genes. RNA hybrids are  
 XX more stable than either hybrids prepared from DNA or single-stranded  
 XX sequences; contain only natural components (so will not induce  
 XX immunological or intolerance reactions) and they enter tumour cells more  
 XX effectively than plasmids. This sequence represents the sequence in the  
 XX wild type human p53 gene around the position of mutation R248Q. The  
 XX oligonucleotides of the invention can be targeted to this sequence.  
 XX Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 16 ATGAACCGGAGG 27  
 3 ATGAACCGGAGG 14  
 RESULT 233  
 ADB54361/c  
 ID ADB54361 standard; DNA; 19 BP.

AC ADB54361;  
 XX 04-DEC-2003 (first entry)  
 XX PCR primer 29 used to amplify genomic DNA region.  
 XX colon cell proliferative disorder; non methylated CpG dinucleotide;  
 XX cytosinetic; cancer; adenoma; carcinoma; cytosine methylation state; ss;  
 XX PCR; primer.  
 XX Unidentified.  
 XX WO2003072821-A2.  
 XX 04-SEP-2003.  
 XX 27-FEB-2003; 2003WO-EP002035.  
 XX 27-FEB-2002; 2002EP-00004551.  
 XX (EPIC-) EPICGENOMICS AG.  
 XX Adorian P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;  
 XX Rujan T, Schmitt A;  
 XX WPI; 2003-731620/69.  
 XX Detecting and differentiating between colon cell proliferative disorders  
 XX associated with a gene or its regulatory regions comprises contacting a  
 XX target nucleic acid in a biological sample obtained from the subject with  
 XX a reagent.  
 XX Claim 15; Page 22; 74pp; English.  
 XX The invention relates to a novel method for detecting and differentiating  
 XX between colon cell proliferative disorders associated with at least one  
 XX gene or its regulatory regions. The method comprises contacting a target  
 XX nucleic acid in a biological sample obtained from the subject with at  
 XX least one reagent or a series of reagents, where the reagent or series of  
 XX reagents, distinguishes between methylated and non methylated CpG  
 XX dinucleotides within the target nucleic acid. The molecules of the  
 XX invention demonstrate cytosinetic activity whilst the method may useful  
 XX for detecting and differentiating between colon cell proliferative  
 XX disorders, including cancers such as colon adenoma and colon carcinoma.  
 XX The RNA (peptide nucleic acid)-oligomers are useful as probes for  
 XX determining cytosine methylation state or single nucleotide  
 XX polymorphisms. The current sequence is that of the PCR primer of the  
 XX invention which was used to amplify the genomic DNA region.  
 XX Sequence 19 BP; 4 A; 0 C; 10 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 9; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 301 AACCCCAACCTC 312  
 12 AACCCCAACCTC 1  
 RESULT 234  
 ADE29549/c  
 ID ADE29549 standard; RNA; 19 BP.  
 AC ADE29549;  
 XX 29-JAN-2004 (first entry)

DE Mitogen activated protein kinase siRNA oligonucleotide SEQ ID NO:171.  
 XX short interfering nucleic acid; siRNA; downregulation; inhibition;  
 XX mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
 XX cytosinetic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;

KW immunosuppressive; antibacterial; antineumatic; antiarthritic;  
 KW antipsoriatic; gastroenteric; obesity; diabetes; tumour;  
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
 KW psoriasis; inflammatory bowel disease; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.  
 OS Synthetic.  
 PN WO2003072590-A1.  
 PD 04-SEP-2003.  
 PF 28-JAN-2003; 2003WO-US002510.  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA Mcswigen J, Belgelman L, Usman N, Haeblerli P, Chowrira B;  
 PI WPI; 2003-689980/65.  
 DR New short interfering nucleic acid, useful e.g. for treatment and  
 XX diagnosis of cancer, downregulates expression of mitogen-activated  
 PT protein kinase genes.  
 PS Example 3; SEQ ID NO 171; 164pp; English.  
 XX The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of a mitogen-activated protein kinase  
 CC (MAPK) genes by RNA interference. Also described: (1) a method for  
 CC modulating expression of MAPK genes in cells, tissue explants or  
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
 CC antiallergic, immunosuppressive, antibacterial, antirheumatic,  
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
 CC disease). They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents a MAPK siNA which is used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 19 BP; 1 A; 10 C; 7 G; 0 T; 1 U; 0 Other;  
 QY Query Match 2.0%; Score 12; DB 9; Length 19;  
 Db Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 381 GCGGCTGCACCG 392  
 19 GCGGCTGCACCG 8  
 RESULT 235  
 ADE29386  
 ID ADE29386 standard; RNA; 19 BP.  
 AC ADE29386;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:8.  
 XX short interfering nucleic acid; siNA; downregulation; inhibition;  
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;  
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antiallergic;  
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;  
 KW antipsoriatic; gastroenteric; obesity; diabetes; tumour;  
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;  
 KW psoriasis; inflammatory bowel disease; drug screening;  
 KW genetic engineering; pharmacogenomic; gene mapping; ss.  
 OS Synthetic.  
 PN WO2003072590-A1.  
 PD 04-SEP-2003.  
 PF 28-JAN-2003; 2003WO-US002510.  
 PR 20-FEB-2002; 2002US-0358580P.  
 PR 11-MAR-2002; 2002US-0363124P.  
 PR 06-JUN-2002; 2002US-0386782P.  
 PR 29-AUG-2002; 2002US-0406784P.  
 PR 05-SEP-2002; 2002US-0408378P.  
 PR 09-SEP-2002; 2002US-0409293P.  
 PR 15-JAN-2003; 2003US-0440129P.  
 XX (SIRN-) SIRNA THERAPEUTICS INC.  
 PA Mcswigen J, Belgelman L, Usman N, Haeblerli P, Chowrira B;  
 PI WPI; 2003-689980/65.  
 DR New short interfering nucleic acid, useful e.g. for treatment and  
 XX diagnosis of cancer, downregulates expression of mitogen-activated  
 PT protein kinase genes.  
 PS Example 3; SEQ ID NO 8; 164pp; English.  
 XX The present invention describes a short interfering nucleic acid (siNA)  
 CC that downregulates expression of a mitogen-activated protein kinase  
 CC (MAPK) genes by RNA interference. Also described: (1) a method for  
 CC modulating expression of MAPK genes in cells, tissue explants or  
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo  
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)  
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs  
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,  
 CC antiallergic, immunosuppressive, antibacterial, antirheumatic,  
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK  
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,  
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I  
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,  
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel  
 CC disease). They can also be used for drug screening; diagnosis; target  
 CC identification and validation; genetic engineering; pharmacogenomics;  
 CC studying gene function and gene mapping (e.g. of single-nucleotide  
 CC polymorphisms). The present sequence represents a MAPK siNA which is used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 19 BP; 1 A; 7 C; 10 G; 0 T; 1 U; 0 Other;  
 QY Query Match 2.0%; Score 12; DB 9; Length 19;  
 Db Best Local Similarity 91.7%; Pred. No. 1.2e+05;  
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 381 GCGGCTGCACCG 392  
 1 GCGGCTGCACCG 12  
 RESULT 236  
 AA052874  
 ID AA052874 standard; RNA; 20 BP.

XX AC AAQ52874;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-MAY-1994 (first entry)  
 XX  
 DE Cytomegalovirus target sequence 51.  
 XX  
 KM RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; hnRNA;  
 KM picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;  
 KM papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;  
 KM T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus;  
 KM influenza virus; HSV; herpes simplex virus; vector; immune response;  
 KM antibody; ribozyme; viral RNA; treatment; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9323569-A1.  
 XX  
 PD 25-NOV-1993.  
 XX  
 PF 29-APR-1993; 93MO-US004020.  
 XX  
 PR 11-MAY-1992; 92US-00882689.  
 PR 14-MAY-1992; 92US-00882712.  
 PR 14-MAY-1992; 92US-00882713.  
 PR 14-MAY-1992; 92US-00882714.  
 PR 14-MAY-1992; 92US-00882823.  
 PR 14-MAY-1992; 92US-00882824.  
 PR 14-MAY-1992; 92US-00882886.  
 PR 14-MAY-1992; 92US-00882888.  
 PR 14-MAY-1992; 92US-00882889.  
 PR 14-MAY-1992; 92US-00882921.  
 PR 14-MAY-1992; 92US-00882922.  
 PR 14-MAY-1992; 92US-00883823.  
 PR 14-MAY-1992; 92US-00883849.  
 PR 14-MAY-1992; 92US-00884079.  
 PR 14-MAY-1992; 92US-00884074.  
 PR 14-MAY-1992; 92US-00884333.  
 PR 14-MAY-1992; 92US-00884422.  
 PR 14-MAY-1992; 92US-00884431.  
 PR 14-MAY-1992; 92US-00884436.  
 PR 14-MAY-1992; 92US-00884521.  
 PR 31-JUL-1992; 92US-00923738.  
 PR 26-AUG-1992; 92US-00935854.  
 PR 18-SEP-1992; 92US-00948355.  
 PR 15-OCT-1992; 92US-00963322.  
 PR 07-DEC-1992; 92US-00987129.  
 PR 07-DEC-1992; 92US-00987130.  
 PR 07-DEC-1992; 92US-00987133.  
 XX  
 PA (RIBO-) RIBOZYME PHARM INC.  
 XX  
 PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecsek JJ;  
 PI Mamone JA;  
 XX  
 DR WPI; 1993-386599/48.  
 XX  
 PT Enzymatic RNA molecules - used to inhibit viral replication, infection  
 PT and gene expression.  
 XX  
 PS Claim 5; Fig 13; 287pp; English.  
 XX  
 CC The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target  
 CC sequences for enzymatic RNA molecules. The RNA molecules are  
 CC complementary to a substrate binding region in the specified gene target.  
 CC They also have enzymatic activity in that they specifically cleave RNA  
 CC in the target. The RMs interfere with viral replication and therefore  
 CC have anti-viral properties. They can be used to attenuate viruses to be  
 CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated  
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct  
 CC PI field.)

XX SQ Sequence 20 BP; 1 A; 9 C; 5 G; 0 T; 5 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 75.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 223 TGCTACCGCGTC 234  
 Db 4 UGCTACCGCGTC 15  
 OY  
 RESULT 237  
 ID AAQ55841 standard; DNA; 20 BP.  
 XX  
 AC AAQ55841;  
 XX  
 DT 21-JUL-1994 (first entry)  
 XX  
 DE HCV detection primer (DNA type 5 S67).  
 XX  
 KM HCV; hepatitis C virus; detection; primer; PCR; mixer primer set;  
 KM polymerase chain reaction; DNA polymerase; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP05337000-A.  
 XX  
 PD 21-DEC-1993.  
 XX  
 PF 04-JUN-1992; 92JP-00168226.  
 XX  
 PR 04-JUN-1992; 92JP-00168226.  
 XX  
 PA (SAYA/) SAYAMA K.  
 XX  
 DR WPI; 1994-037380/05.  
 XX  
 PT Detection of type C hepatitis virus - using one step DNA polymerase chain  
 PT reaction with mixed primer set.  
 XX  
 PS Claim 2; Page 2; 7pp; Japanese.  
 XX  
 CC The primers (AAQ55811-841) are used to detect various types of hepatitis  
 CC C virus. The primers are made from oligo DNA fragments selected from  
 CC specific hepatitis C virus subtypes. The primers can be used to in a one  
 CC step PCR reaction which can determine the subtypes of a large number of  
 CC samples  
 XX  
 SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;  
 SQ  
 Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 36 TTACCAATTCAA 47  
 Db 8 TTACCAATTCAA 19  
 OY  
 RESULT 238  
 ID AAQ94258/c  
 XX  
 AC AAQ94258;  
 XX  
 DT 05-DEC-1995 (first entry)  
 XX  
 DE Antisense primer to amplify 429 bp SV40 large T antigen gene fragment.  
 XX  
 KM primer; PCR; polymerase chain reaction; SV40; large T antigen;  
 KM mouse hepatoma cell; animal model; cancer; ss.

```

XX OS Synthetic.
XX PS JP07079773-A.
XX PN 28-MAR-1995.
XX PD 19-JUL-1994; 94JP-00166647.
XX PF 20-JUL-1993; 93JP-00179402.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX PS WPI; 1995-157844/21.
XX PT Mouse hepatoma cell line - useful in animal model systems of cancer.
XX PS Example; Page 4; 5pp; Japanese.
XX CC This antisense primer was used in PCR, with the sense primer shown in
CC AAQ94257, to amplify a region from nucleotides 1571 to 2009 of the SV40
CC large T antigen gene. A fragment of 429 bp was generated. The fragment is
CC used in the invention, a mouse hepatoma cell line which may metastasise
CC specifically in the liver and contains an albumin promoter gene and a
CC SV40-T gene. The cell line is useful for the production of animal models
CC for the study of cancer and screening of anti-cancer agents
XX SQ Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 423 CAAGATATTT 434
DB 18 CAAGATATTT 7

RESULT 239
AAQ91041/c
ID AAQ91041 standard; DNA; 20 BP.
XX AC AAQ91041;
XX DT 30-JAN-1996 (first entry)
XX DE HHV-6 associated MS genetic marker MDPB internal primer MSHind9.
XX KW Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; MDPB;
XX internal primer MSHind9; diagnosis; ss.
XX OS Synthetic.
XX PN WO9512313-A1.
XX PD 11-MAY-1995.
XX PF 04-NOV-1994; 94WO-US012655.
XX PR 05-NOV-1993; 93US-00149176.
XX PR 24-MAR-1994; 94US-00218029.
XX PR 05-AUG-1994; 94US-00287942.
XX PR 04-NOV-1994; 94US-00334482.
XX PA (PATH-) PATHOGENESIS CORP.
XX PI Burner GC, Chailoner PB, Smith KT, Brown JP, Parker JD;
XX PI Nowinski RC;
XX DR WPI; 1995-215032/28.
XX PT Treatment of human herpes-virus-6-associated multiple sclerosis - using
XX an antiviral agent, e.g. a nucleoside analogue, administered to the

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PT cerebrospinal fluid.
XX PS Disclosure; Page 34; 11pp; English.
XX PN AAQ91041 and AAQ91042 are an internal primer pair for the human herpes
XX virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, MDPB
XX (AAQ91043). The primers can be used in the diagnosis of MS
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 TCGGCGTGAGAC 80
DB 17 TCGGCGTGAGAC 6

RESULT 240
AAT08653/c
ID AAT08653 standard; DNA; 20 BP.
XX AC AAT08653;
XX DT 05-SEP-1996 (first entry)
XX DE Primer p53-SX6MP for p53 gene exon 6 amplification.
XX KW primer; PCR; polymerase chain reaction; hierarchy; immunoassay;
XX quantitative assay; fragment length; DNA sequencing; p53; mutation; ss.
XX OS Synthetic.
XX PN WO9601909-A1.
XX PD 25-JAN-1996.
XX PF 07-JUL-1995; 95WO-US008605.
XX PR 08-JUL-1994; 94US-00271946.
XX PR 14-FEB-1995; 95US-00388381.
XX PA (VISI-) VISIBLE GENETICS INC.
XX PI Diamandis E, Dunn JM, Stevens JK;
XX DR WPI; 1996-097638/10.
XX PT Testing for disease-associated p53 gene mutation(s) using a hierarchy of
XX assay techniques - e.g. immunoassay, DNA amplification and DNA
XX sequencing.
XX PS Claim 18; Page 21; 44pp; English.
XX CC Rapid and cost effective diagnosis of disease-associated mutations in the
XX p53 gene is achieved by employing a selected number of diagnostic tools,
XX in a hierarchy of increasing accuracy and cost per tool, in which each
XX tool detects essentially no false positives. Tests that may be employed,
XX in order of increasing accuracy and cost are: (a) immunoassays; (b) DNA
XX fragment length/quantity analysis; and (c) DNA sequencing of regions
XX most likely to harbour point mutations. AAT08645-66 are primers used in
XX DNA fragment length/quantity analysis. The amplification of the eleven
XX exons is advantageously carried out in 3 multiplex pools, the members of
XX a pool selected because they all use the same hybridisation temperature
XX and none of the expected fragment lengths will overlap in an
XX electrophoresis gel. One of each pair of primers is labeled at the 5' end
XX with an identifiable marker such as fluorescein, rhodamine or cyanine.
XX The present sequence is used with AAT08654 to amplify a 247 bp fragment
XX of exon 6
XX SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

```

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
 |||||  
 DB 18 TCGTCTCTCCAG 7

## RESULT 241

AA08652  
 ID AA08652 standard; DNA; 20 BP.

XX  
 AC AA08652;  
 XX  
 DT 05-SEP-1996 (first entry)  
 XX  
 DE Primer p53-3X5MP for p53 gene exon 5 amplification.  
 XX

KM primer; PCR; polymerase chain reaction; hierarchy; immunoassay;  
 KM quantitative assay; fragment length; DNA sequencing; p53; mutation; ss.

XX  
 OS Synthetic.  
 XX  
 PN MO9601909-A1.  
 XX

PD 25-JUN-1996.

XX  
 PF 07-JUL-1995; 95WO-US008605.  
 XX

PR 08-JUL-1994; 94US-00271946.  
 PR 14-FEB-1995; 95US-00386381.  
 XX

PA (VISI-) VISIBLE GENETICS INC.

PI Diamandis E, Dunn JM, Stevens JK.  
 XX

DR WPI; 1996-097638/10.  
 XX

PT Testing for disease-associated p53 gene mutation(s) using a hierarchy of  
 PT assay techniques - e.g. immunoassay, DNA amplification and DNA  
 PT sequencing.

PS Claim 18; Page 21; 44pp; English.

XX  
 CC Rapid and cost effective diagnosis of disease-associated mutations in the  
 CC p53 gene is achieved by employing a selected number of diagnostic tools,  
 CC in a hierarchy of increasing accuracy and cost per tool, in which each  
 CC tool detects essentially no false positives. Tests that may be employed,  
 CC in order of increasing accuracy and cost are: (a) immunoassays; (b) DNA  
 CC fragment length/quantity analysis; and (c) DNA sequencing of regions  
 CC most likely to harbour point mutations. AA08645-66 are primers used in  
 CC DNA fragment length/quantity analysis. The amplification of the eleven  
 CC exons is advantageously carried out in 3 multiplex pools, the members of  
 CC a pool selected because they all use the same hybridisation temperature  
 CC and none of the expected fragment lengths will overlap in an  
 CC electrophoresis gel. One of each pair of primers is labeled at the 5' end  
 CC with an identifiable marker such as fluorescein, rhodamine or cyanine.  
 CC The present sequence is used with AA08651 to amplify a 268 bp fragment  
 CC of exon 5  
 CC

XX  
 SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
 |||||  
 DB 9 TCGTCTCTCCAG 20

## RESULT 242

AA09864/c  
 ID AA09864 standard; DNA; 20 BP.

XX  
 AC AA09864;  
 XX

DT 07-MAY-1998 (first entry)  
 XX

DE Primer for exon 6 of p53 gene.

KM PCR primer; amplify; pathogen identification; mutation detection;  
 KM nucleic acid analysis; microorganism characterisation; human;  
 KM HLA type determination; p53 gene exon 6; ss.

XX  
 OS Synthetic.  
 XX  
 PN Homo sapiens.  
 PN MO9741259-A1.  
 XX

PD 06-NOV-1997.

XX  
 PF 29-APR-1997; 97WO-US007135.  
 XX

PR 01-MAY-1996; 96US-00640672.  
 PR 19-JUL-1996; 96US-00684498.  
 PR 27-FEB-1997; 97US-00807138.  
 XX

PA (VISI-) VISIBLE GENETICS INC.

PI Leshner J, Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R;  
 XX

DR WPI; 1997-549755/50.  
 XX

PT Nucleic acid sequence determination - comprising synthesising chain  
 PT extension products, which are indicative of positions of selected species  
 PT of nucleotide in nucleotide sequence.

PS Example 4; Page 19; 69pp; English.

XX  
 CC This sequence represents a primer for exon 6 of the p53 gene. This  
 CC sequence can be used in the method of the invention for determining the  
 CC position of at least one selected species of nucleotide, in a region of  
 CC interest, in a target nucleic acid polymer, in a sample. The method  
 CC comprises combining the sample with a reaction mixture to synthesise  
 CC chain extension products indicative of the positions of the species of  
 CC nucleotide in the region of interest and evaluating the products  
 CC produced, characterised in that the sample, which is combined with the  
 CC reaction mixture, and contains target and non-target nucleic acid  
 CC polymers in natural abundance. The method can be used to detect  
 CC mutations, particularly mutations of medical significance, in samples  
 CC derived from a human patient, animal, plant or microorganism, determine  
 CC HLA type ancillary to transplant procedures, detect and identify  
 CC microorganisms, particularly pathogenic microorganisms, in a sample and  
 CC in situ sequencing reactions to produce sequencing fragments in a  
 CC histological specimen  
 CC

XX  
 SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
 |||||  
 DB 18 TCGTCTCTCCAG 7

## RESULT 243

AA09863  
 ID AA09863 standard; DNA; 20 BP.

XX  
 AC AA09863;  
 XX

DT 07-MAY-1998 (first entry)

```

XX DE Primer for exon 5 of p53 gene.
XX
XX PCR primer; amplify; pathogen identification; mutation detection;
XX KW nucleic acid analysis; microorganism characterisation; human;
XX KW HLA type determination; p53 gene exon 5; ss.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX EN WO9741259-A1.
XX
XX PD 06-NOV-1997.
XX
XX PF 29-APR-1997; 97WO-US007135.
XX
XX PR 01-MAY-1996; 96US-00640672.
XX PR 19-JUL-1996; 96US-00684498.
XX PR 27-FEB-1997; 97US-00807138.
XX
XX PA (VISTA) VISIBLE GENETICS INC.
XX
XX PI Leusiner J, Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R;
XX
XX DR WPI; 1997-549755/50.
XX
XX PT Nucleic acid sequence determination - comprising synthesising chain
XX PT extension products, which are indicative of positions of selected species
XX PT of nucleotide in nucleotide sequence.
XX
XX PS Example 4; Page 19; 69pp; English.
XX
XX CC This sequence represents a primer for exon 5 of the p53 gene. This
XX CC sequence can be used in the method of the invention for determining the
XX CC position of at least one selected species of nucleotide, in a region of
XX CC interest, in a target nucleic acid polymer, in a sample. The method
XX CC comprises combining the sample with a reaction mixture to synthesise
XX CC chain extension products indicative of the positions of the species of
XX CC nucleotide in the region of interest and evaluating the products
XX CC produced, characterised in that the sample, which is combined with the
XX CC reaction mixture, and contains target and non-target nucleic acid
XX CC polymers in natural abundance. The method can be used to detect
XX CC mutations, particularly mutations of medical significance, in samples
XX CC derived from a human patient, animal, plant or microorganism, determine
XX CC HLA type ancillary to transplant procedures, detect and identify
XX CC microorganisms, particularly pathogenic microorganisms, in a sample and
XX CC in situ sequencing reactions to produce sequencing fragments in a
XX CC histological specimen
XX
XX SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 TCCTCTCTCCAG 521
XX |||||
XX Db 9 TCCTCTCTCCAG 20
XX
XX RESULT 244
XX AAT79479/c
XX ID AAT79479 standard; DNA; 20 BP.
XX
XX AC AAT79479;
XX
XX XX 22-OCT-1997 (first entry)
XX
XX DE DNA ligand for adenosine or adenosine 5'-phosphate.
XX
XX KW Adenosine; adenosine-5'-phosphate; adenosine triphosphate; ATP; binding;
XX KW ligand; purification; reagent; isolation; determination;
XX KW subcellular localisation; catalyst; assay; SELEX;

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XX KW Systematic Evolution of Ligands by Exponential enrichment; ss.
XX
XX OS Synthetic.
XX
XX PN US631146-A.
XX
XX PD 20-MAY-1997.
XX
XX PF 19-JAN-1995; 95US-00375116.
XX
XX PR 19-JAN-1995; 95US-00375116.
XX
XX PA (GENO) GEN HOSPITAL CORP.
XX
XX PI Szostak JM, Huizenga DE;
XX
XX DR WPI; 1997-288574/26.
XX
XX PT Single stranded DNA molecule, which binds adenosine or adenosine-5'-
XX PT phosphate - useful as purification reagent, or for determination of
XX PT adenosine triphosphate subcellular localisation in vivo.
XX
XX PS Claim 3; Col 63-64; 55pp; English.
XX
XX CC The present sequence is an adenosine or adenosine-5'-phosphate (ASP)
XX CC binding single stranded DNA molecule, which can be used as a purification
XX CC reagent for the isolation of adenosine or an ASP, or to determine the
XX CC subcellular localisation of, e.g. adenosine triphosphate (ATP), in vivo.
XX CC The DNA molecule was prepared by contacting DNA molecules having a region
XX CC of random sequence with adenosine or ASP (preferably ATP), isolating a
XX CC subpopulation by partitioning DNA molecules which specifically bind the
XX CC adenosine or ASP, amplifying the subpopulation in vitro and repeating the
XX CC process 4 times to obtain a single stranded DNA molecule capable of
XX CC binding adenosine or ASP, i.e. Systematic Evolution of Ligands by
XX CC Exponential enrichment (SELEX). Catalytic DNA produced using the method
XX CC can be used as in vitro or in vivo catalysts, or to detect the presence
XX CC of the ligand. They may also be used in assays to detect molecules
XX CC modified by the DNA, which are not themselves ligands, e.g. DNA
XX CC phosphorylated by a polynucleotide kinase catalyst. The DNA molecule has
XX CC significant advantages over ligand binding and catalytic RNA in terms of
XX CC stability and synthesis cost
XX
XX SQ Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 180 CTTCCTCCGCTA 191
XX |||||
XX Db 16 CTTCCTCCGCTA 5
XX
XX RESULT 245
XX AAT91100
XX ID AAT91100 standard; DNA; 20 BP.
XX
XX AC AAT91100;
XX
XX XX 27-MAR-1998 (first entry)
XX
XX DE Bovine lysosomal alpha-mannosidase (LAMAN) gene PCR primer mp5UTIF.
XX
XX KW LAMAN; lysosomal alpha-mannosidase; alpha-mannosidosis; cattle;
XX KW diagnosis; screening; genetic test; PCR; primer; RFLP;
XX KW restriction fragment length polymorphism; ss.
XX
XX OS Synthetic.
XX OS Bos taurus.
XX
XX PN WO9726369-A1.
XX
XX PD 24-JUL-1997.

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XX PF 15-JAN-1997; 97WO-GB000109.
XX PR 15-JAN-1996; 96NO-00000163.
XX PA (HEAL/) HEALY P.
XX PA (DZIE/) DZIEGLEWSKA H.
XX PI Berg T, Tollersrud OK, Nilsen O;
XX DR WPI; 1997-385352/35.
XX PT Diagnosis and screening for bovine alpha-mannosidosis - by detecting
XX PT mutations in alpha-mannosidase gene, also nucleic acid encoding the
XX PT enzyme and derived oligo:nucleotide primers.
XX PS Example 2; Page 22; 85pp; English.
XX CC Forward primer mp5UTP is based on a 1500 bp amplicon produced from
XX CC bovine fibroblast genomic DNA using primers (see AAT91098-99) based on
XX CC the bovine alpha-mannosidase (LAMN) gene (see AAT91086). It was used
XX CC with reverse primer mp262 (see AAT91101) to obtain an 800 bp RT-PCR
XX CC product that constituted a 5' part of LAMN cDNA. This was combined with
XX CC a previously obtained PCR cDNA fragment (see AAT91096-97) to produce a
XX CC full-length clone (see AAT91086) for LAMN (see AAT26682). Mutations in
XX CC the LAMN gene cause bovine alpha-mannosidosis, and can be detected using
XX CC claimed PCR primers (see AAT91088-93)
XX SQ Sequence 20 BP; 2 A; 5 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 GCGGCGGCTGCA 389
DB 7 GCGGCGGCTGCA 18

RESULT 246
AAT9833
ID AAT9833 standard; DNA; 20 BP.
XX AC AAT9833;
XX OS Synthetic.
XX OS Homo sapiens.
XX OS WO9741258-A1.
XX PN WO9741258-A1.
XX PD 06-NOV-1997.
XX PF 29-APR-1997; 97WO-US007134.
XX PR 01-MAY-1996; 96US-00640672.
XX PR 19-JUL-1996; 96US-00684498.
XX PA (VIST-) VISIBLE GENETICS INC.
XX PI Leushner J, Hui M, Dunn JM, Larson MT, Lacroix J;
XX DR WPI; 1997-549754/50.
XX PT Amplifying nucleic acid containing sample - comprises performing multiplex
XX PT amplification reaction and reacting amplified fragments in sequencing

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PT reaction mixture.
XX PF Example 4; Page 18; 37pp; English.
XX CC This sequence represents a primer for exon 5 of the p53 gene. This
XX CC sequence can be used in the method of the invention for analyzing a
XX CC nucleic acid containing sample. The method comprises performing a
XX CC multiplex amplification reaction on the nucleic acids in the sample using
XX CC amplification primer pairs, one pair for each region to be analysed, to
XX CC produce a mixture of amplified fragments, and determining the sequence of
XX CC at least one species of amplified fragment, characterised in that the
XX CC sequence is determined by combining the mixture of amplification
XX CC fragments with a sequencing reaction mixture for the production of
XX CC sequencing fragments, and evaluating the sequencing fragments produced.
XX CC The method can be used to analyse regions in the nucleic acids in the
XX CC sample for the presence of mutations, or detect and type microorganisms.
XX CC The method directly performs sequencing reactions on complex DNA mixtures
XX SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
DB 9 TCGTCTCTCCAG 20

RESULT 247
AAT9834/C
ID AAT9834 standard; DNA; 20 BP.
XX AC AAT9834;
XX OS Synthetic.
XX OS Homo sapiens.
XX OS WO9741258-A1.
XX PN WO9741258-A1.
XX PD 06-NOV-1997.
XX PF 29-APR-1997; 97WO-US007134.
XX PR 01-MAY-1996; 96US-00640672.
XX PR 19-JUL-1996; 96US-00684498.
XX PA (VIST-) VISIBLE GENETICS INC.
XX PI Leushner J, Hui M, Dunn JM, Larson MT, Lacroix J;
XX DR WPI; 1997-549754/50.
XX PT Amplifying nucleic acid containing sample - comprises performing multiplex
XX PT amplification reaction and reacting amplified fragments in sequencing
XX PT reaction mixture.
XX PS Example 4; Page 18; 37pp; English.
XX CC This sequence represents a primer for exon 6 of the p53 gene. This
XX CC sequence can be used in the method of the invention for analysing a
XX CC nucleic acid containing sample. The method comprises performing a
XX CC multiplex amplification reaction on the nucleic acids in the sample using
XX CC amplification primer pairs, one pair for each region to be analysed, to
XX CC produce a mixture of amplified fragments, and determining the sequence of

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at least one species of amplified fragment, characterised in that the sequence is determined by combining the mixture of amplification fragments with a sequencing reaction mixture for the production of sequencing fragments, and evaluating the sequencing fragments produced. The method can be used to analyse regions in the nucleic acids in the sample for the presence of mutations, or detect and type microorganisms. The method directly performs sequencing reactions on complex DNA mixtures.

Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

510 TCCTCTCTCCAG 521  
18 TCCTCTCTCCAG 7

RESULT 248  
AAV47975  
ID AAV47975 standard; DNA; 20 BP.

AAV47975;  
19-OCT-1998 (first entry)

Human B7-2 targeted oligonucleotide 10371.

ss; human; B7; T cell; inflammation; autoimmune disease; cell activation; cell proliferation.

Synthetic.  
Homo sapiens.

Key Location/Qualifiers  
modified\_base 1.20  
/\*tag= a  
/note= "Phosphorothioate linkages"

MO9829124-A1.

09-JUL-1998.

16-DEC-1997; 97MO-US023270.

31-DEC-1996; 96US-00777266.

(ISIS-) ISIS PHARM INC.

Bennett CF, Vickers TA;

WFI; 1998-387783/33.

New oligo:nucleotide(s) that modulate expression of B7 proteins - used for, e.g. controlling activation and proliferation of T cells, particularly for treatment, diagnosis and prevention of inflammation.

Example 1; Page 38; 120pp; English.

The oligonucleotides which specifically hybridise to B7 modulate its expression (and thus T cell activation and proliferation). This is particularly useful for treatment and prevention of inflammation and autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis, Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis, (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis, rhinitis, allergy, cancer and metastases. The oligonucleotides may also be used to manipulate T cell activation ex vivo; to determine or detect B7 protein expression; for diagnosis; as assay and purification reagents, and to study physiological roles of B7 proteins

Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 TCCTGAGAGCCG 258  
6 TCCTGAGAGCCG 17

RESULT 249

AAV55998  
ID AAV55998 standard; DNA; 20 BP.

AAV55998;

04-DEC-1998 (first entry)

GTPCH-1 mRNA amplifying RT-PCR primer 19c1.

Selective inhibitor; nitric oxide synthase; NOS; tetrahydrobiopterin; THB; GTP cyclohydrolase 1; nitric oxide; septic shock; asthma; arthritis; inflammatory bowel disease; heart failure; acute systemic inflammation; neurological disease state; neuronal NOS; dementia; Parkinson's disease; stroke; RT-PCR; GTPCH-1; primer; ss.

Synthetic.  
Homo sapiens.

WO9835055-A1.

13-AUG-1998.

05-FEB-1998; 98MO-GB000353.

05-FEB-1997; 97GB-00002312.

(UNLO) UNIV COLLEGE LONDON.

Charles IG, Bhagat K, Vallance PJ, Hingorani AD;

WFI; 1998-542240/46.

Identification of selective inhibitors of nitric oxide synthases - by determining inhibition of enzyme activity in presence of candidate compound and varying concentrations of tetrahydrobiopterin.

Example; Page 13; 30pp; English.

Sequences shown in AAV55996 to AAV56003 represent primers used for RT-PCR amplification during the course of the invention. The invention provides a method for identification of selective inhibitors of nitric oxide synthases (NOS) which comprises determining inhibition of activity of NOS in the presence of a candidate compound and two different concentrations of tetrahydrobiopterin (THB). Inhibitor of GTP cyclohydrolase 1-mediated synthesis of THB can be identified by contacting GTP cyclohydrolase 1 with a candidate compound and determining inhibition of the enzyme mediated synthesis of THB by the candidate compound. The inhibitors identified by the methods may be used in treatment of conditions in which the production of nitric oxide (NO) is implicated, such as septic shock, asthma, arthritis, inflammatory bowel disease, heart failure or acute systemic inflammation. The inhibitors may also be useful in treatment of neurological disease states in which neuronal NOS has been implicated, e.g. stroke, dementia or Parkinson's disease

Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred.No.1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

137 TTGGTATCTTC 148  
1 TTGGTATCTTC 12



DR WPI; 1999-070222/06.  
XX  
XX Differentiating products from different animal breeds - by the analysis  
PT of alleles of breed-determinant genes, at the nucleic acid or protein  
PT level.  
XX  
XX Example 22; Page 70; 101pp; English.  
PS  
CC A method has been developed for: (a) differentiating animals and animal  
CC products according to breed origin; (b) determining or testing the breed  
CC origin of a product; or (c) validating an animal product. The method  
CC comprises analysing a sample of the product for the allele(s) of at least  
CC one breed-determinant (BD) gene. The present invention also describes:  
CC (i) methods for determining the coat colour genotype of a pig by  
CC determining: (i) the allele(s) of the alpha melanocyte-stimulating  
CC hormone receptor (alpha-MSHR) gene; (ii) the amino acid sequence of an  
CC alpha-MSHR protein at positions associated with coat colour, or the size  
CC of the protein; (iii) detecting which microsatellites (or other linked  
CC marker alleles), linked to the alpha-MSHR gene, or particular alleles of  
CC it, are present; and (iv) analysing nucleic acid to determine if the KIT  
CC gene carries a polymorphism associated with the Belt genotype. The main  
CC method of the invention is applied to samples from fish, birds and  
CC mammals, especially pigs. Particular applications are confirming stated  
CC origin of meats; in quality control; for maintaining stock purity, and in  
CC breeding programmes (to confirm particular crosses). The method requires  
CC only very small samples and many samples can be screened quickly and  
CC inexpensively. The process can be made quantitative. The present sequence  
CC represents an alpha-MSHR PCR primer from the present invention  
XX  
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;  
Query Match 2.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 243 CACCTCTCTGAG 254  
DB 20 CACCTCTCTGAG 9  
RESULT 253  
AA90393  
ID AAX90393 standard; DNA; 20 BP.  
XX  
AC AAX90393;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Human p53 gene reverse transcription PCR primer exon 5 antisense.  
XX  
XX Human; p53; reverse transcription; PCR primer; cancer; diagnosis; mutant;  
XX cyclin-dependent kinase; CDK; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN GB2334578-A.  
XX  
PD 25-AUG-1999.  
XX  
PF 18-FEB-1998; 98GB-00003447.  
XX  
PR 18-FEB-1998; 98GB-00003447.  
XX  
PA (UTLI-) UNIV LIVERPOOL.  
XX  
XX Warenus HM; Seabra L;  
XX  
XX WPI; 1999-432548/37.  
XX  
PT Diagnosis of cancerous or pre-cancerous cells by monitoring the levels of  
PT cyclin-dependent kinases 1 and 4.  
XX

PS Example; Page 12; 26pp; English.  
XX  
CC The present invention describes a method for the diagnosis of a cancerous  
CC or pre-cancerous state from the co-elevation of cyclin-dependent kinase 1  
CC (CDK1) and CDK4 levels. The method may be used for the clinical diagnosis  
CC of cancerous or pre-cancerous cells. In addition the combination of  
CC targets may be used to screen for drugs that may specifically act on  
CC cancer cells. The combination of CDK1, CDK4 elevation and p53 mutation in  
CC combination form a complex target that is likely to be specific for  
CC cancerous cells. AAX90388 to AAX90401 represent reverse transcription PCR  
CC primer for the human p543 gene, used in an example from the present  
CC invention  
XX  
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;  
Query Match 2.0%; Score 12; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 510 TCGTCTCTCCAG 521  
DB 9 TCGTCTCTCCAG 20  
RESULT 254  
AA90379  
ID AAX90379 standard; DNA; 20 BP.  
XX  
AC AAX90379;  
XX  
DT 24-SEP-1999 (first entry)  
XX  
DE Human p53 gene reverse transcription PCR primer exon 5 antisense.  
XX  
XX Human; p53; reverse transcription; PCR primer; cancer; cytotoxic;  
XX signal transduction factor; mutant; cell cycle; apoptosis; chemotherapy;  
XX ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN GB2334579-A.  
XX  
PD 25-AUG-1999.  
XX  
PF 03-JUL-1998; 98GB-00014545.  
XX  
PR 18-FEB-1998; 98GB-00003446.  
XX  
PR 18-FEB-1998; 98GB-00003447.  
XX  
PR 05-JUN-1998; 98GB-00012151.  
XX  
PA (UTLI-) UNIV LIVERPOOL.  
PA (THER-) THERYTE LTD.  
XX  
XX Warenus HM; Seabra LA;  
XX  
XX WPI; 1999-422071/36.  
XX  
PT Determination of sensitivity of cancer cells to anti-cancer agents.  
XX  
PS Example 1; Page 18; 46pp; English.  
XX  
CC The present invention describes a method for the determination of  
CC sensitivity of cancer cells to anti-cancer agents by measuring the  
CC mutational status, expression and/or function of signal transduction  
CC factors. The method, by measuring the resistance of cells to anti-cancer  
CC agents, is useful for selecting the most appropriate therapy for patients  
CC suffering from cancer. AAX90374 to AAX90387 represent reverse  
CC transcription PCR primer for the human p543 gene, used in an example from  
CC the present invention  
XX  
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521  
 |||||  
 Db 9 TCGTCTCTCCAG 20

RESULT 255  
 AAZ00491  
 ID AAZ00491 standard; DNA; 20 BP.  
 XX  
 AC AAZ00491;  
 XX  
 DT 06-OCT-1999 (first entry)  
 XX  
 DE Human thiorredoxin DNA binding antisense oligonucleotide 2614.  
 XX  
 KM Thiorredoxin; thiorredoxin reductase; human; antisense; primer; metastasis;  
 KW cytoskeletal; tumour growth inhibitor; detection; nuclease resistant;  
 KM phosphorothioate linkage; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO938963-A1.  
 XX  
 PD 05-AUG-1999.  
 XX  
 PF 29-JUN-1999; 99WO-CA000077.  
 XX  
 PR 30-JAN-1998; 98US-0073196P.  
 XX  
 PA (GENE-) GENESENSE TECHNOLOGIES INC.  
 XX  
 PI Wright JA, Young AH, Lee YS;  
 PI WPI; 1999-469328/39.  
 XX  
 DR WPI; 1999-469328/39.  
 XX  
 PT Antisense oligonucleotides against thiorredoxin and thiorredoxin reductase  
 gene, useful for inhibiting tumor growth and metastasis.  
 XX  
 PS Claim 1; Page 18; 88pp; English.  
 XX  
 CC This invention describes novel antisense oligonucleotides against  
 CC thiorredoxin and thiorredoxin reductase gene which have cytostatic activity  
 CC and are useful for inhibiting tumour growth and metastasis in mammals.  
 CC They may also be used as hybridization probes to detect the presence of  
 CC the thiorredoxin and thiorredoxin reductase mRNAs in mammalian cells. They  
 CC may also be used as molecular weight markers. The antisense  
 CC oligonucleotides are nuclease resistant due to the presence of  
 CC phosphorothioate internucleotide linkages. AAZ00478-200503 represent  
 CC oligonucleotide primers capable of binding to human thiorredoxin mRNA  
 XX  
 SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TCGAATACCTTT 453  
 |||||  
 Db 7 TCGAATACCTTT 18

RESULT 256  
 AAX79784  
 ID AAX79784 standard; DNA; 20 BP.  
 XX  
 AC AAX79784;  
 XX  
 DT 17-AUG-1999 (first entry)

XX  
 XX PCR primer H16016 for mitochondrial DNA analysis.  
 DE  
 XX  
 KW PCR primer; human; mitochondrial DNA; genetic diagnosis;  
 KW adult disease contraction; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN JP11113597-A.  
 XX  
 PD 27-APR-1999.  
 XX  
 PF 13-OCT-1997; 97JP-00279127.  
 XX  
 PR 13-OCT-1997; 97JP-00279127.  
 XX  
 PA (TANAKA/) TANAKA M.  
 XX  
 DR WPI; 1999-320841/27.  
 XX  
 PT Genetic diagnosis using human mitochondrial DNA - comprises detecting  
 base replacements.  
 XX  
 PS Example 2; Page 6; 15pp; Japanese.  
 XX  
 CC This sequence represents a PCR primer that can be used in the method of  
 CC the invention. The method is for genetic diagnosis using human  
 CC mitochondrial DNA where there is at least one base replacement from among  
 CC the following five replacements: the 3010th base is changed from guanine  
 CC to adenine; the 4883rd base from cytosine to thymine; the 5178th base  
 CC from cytosine to adenine; the 8414th base from cytosine to thymine; and  
 CC the 14688th base from cytosine to thymine. The method can be used for  
 CC diagnosing the probability of contracting adult diseases. A confirmation  
 CC of base replacement can give a diagnosis of the level of probability of  
 CC contraction of adult diseases  
 XX  
 SQ Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 CCATGAAGAGAC 473  
 |||||  
 Db 2 CCATGAAGAGAC 13

RESULT 257  
 AAX92037  
 ID AAX92037 standard; DNA; 20 BP.  
 XX  
 AC AAX92037;  
 XX  
 DT 13-SEP-1999 (first entry)  
 XX  
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.  
 XX  
 KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
 KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
 KW neutralising epitope; PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Chlamydia pneumoniae.  
 XX  
 PN WO9927105-A2.  
 XX  
 PD 03-JUN-1999.  
 XX  
 PF 20-NOV-1998; 98WO-IB001890.  
 XX  
 PR 21-NOV-1997; 97FR-00014673.  
 XX  
 DT 04-NOV-1998; 98US-0107078P.

```

XX (GEST ) GENSET.
XX
XX Grifflais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
XX Page 1480; Disclosure; 1912pp; English.
XX
XX AAX91991-X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY3584 - AAY3587) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 316 CTGAGATCTTC 327
XX
XX Db 9 CTGAGATCTTC 20
XX
XX RESULT 258
XX AAC61817/C
XX ID AAC61817 standard; DNA; 20 BP.
XX
XX AAC61817;
XX
XX 06-MAR-2001 (first entry)
XX
XX Antisense oligonucleotide directed against human Fas (Apo-1) gene.
XX
XX Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;
XX Fas associated protein 1; protein tyrosine phosphatase; cancer;
XX autoimmune disease; inflammatory disease; lymphoma; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX misc_feature 1..20
XX /*tag= b
XX /note= "contains phosphorothioate linkages"
XX
XX modified_base 1..5
XX /*tag= a
XX /note= "2'-methoxyethoxy residues"
XX
XX modified_base 16..20
XX /*tag= c
XX /note= "2'-methoxyethoxy residues"
XX
XX WO200061150-A1.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US009540.
XX
XX 12-APR-1999; 99US-00290640.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM, Marcusson Eg,
XX

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XX WPI; 2000-628395/60.
XX
XX Antisense oligonucleotides for treating hepatitis and colon, liver or
XX lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein 1
XX (Fap-1) expression.
XX
XX Claim 3; Page 45; 116pp; English.
XX
XX AAC61799-C61819 represent antisense oligonucleotides which are directed
XX against nucleic acid compounds encoding human Fas (Apo-1). The specification
XX describes antisense compounds which are targeted to the 5'-untranslated
XX region, translational start site, translational termination region or 3'-
XX untranslated region of nucleic acid molecules encoding Fas, Fas ligand
XX (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
XX phosphatase). The antisense compounds are used to inhibit the expression
XX of Fas, FasL or Fap-1 in cells or tissues. They are used to treat
XX autoimmune or inflammatory diseases such as hepatitis. They can also be
XX used to treat cancer, especially colon, liver or lung cancer or lymphoma
XX
XX Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 171 GAATTGCTCTT 182
XX
XX Db 20 GAATTGCTCTT 9
XX
XX RESULT 259
XX AAA37589
XX ID AAA37589 standard; DNA; 20 BP.
XX
XX AAA37589;
XX
XX 15-AUG-2000 (first entry)
XX
XX Antisense sequence #47 used to inhibit telomerase activity.
XX
XX Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
XX inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
XX AIDS; HIV; fungal infection; forensic identification; detect; tumour;
XX paternity testing; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_feature 1..20
XX /*tag= a
XX /note= "Phosphorothioate internucleotide linkages"
XX
XX US6046307-A.
XX
XX 04-APR-2000.
XX
XX 09-APR-1997; 97US-00838545.
XX
XX 09-APR-1996; 96US-00630019.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
XX
XX Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;
XX
XX WPI; 2000-292432/25.
XX
XX New peptide nucleic acid (PNA) compounds that inhibit telomerase activity
XX in mammalian cells is useful as probes to detect the RNA component of a
XX mammalian telomerase.
XX
XX Example 1; Col 29; 45pp; English.
XX

```

CC The present sequence represents an antisense oligonucleotide used as a  
 CC control sequence alongside a peptide nucleic acid molecule which  
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (htr) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on htr gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component

Query Match 2.0%; Score 12; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330  
 |||||  
 Db 1 AGGATCTTCACC 12

RESULT 260  
 AAA37584  
 ID AAA37584 standard; DNA; 20 BP.

AC AAA37584;  
 DT 15-AUG-2000 (first entry)

DE PNA sequence #42 used to inhibit telomerase activity.

KM Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;  
 KM inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;  
 KM AIDS; HIV; fungal infection; forensic identification; detect; tumour;  
 KM paternity testing; ss.

OS Synthetic.

Key Location/Qualifiers  
 misc\_feature 1..20

FT /note= "Peptide nucleic acid molecule, where N-(2-  
 FT aminoethyl)glycine units are linked to nucleoside bases  
 FT via glycine amino N through a methylenecarbonyl linker"

US6046307-A.

04-APR-2000.

09-APR-1997; 97US-00838545.

XX

PR 09-APR-1996; 96US-00630019.  
 XX (TEXA) UNIV TEXAS SYSTEM.  
 PA  
 PI Wright WE, Piatyzek MA, Shay JW, Norton JC, Corey DR;  
 XX WPI; 2000-292432/25.  
 DR  
 XX  
 PT New peptide nucleic acid (PNA) compounds that inhibit telomerase activity  
 PT in mammalian cells is useful as probes to detect the RNA component of a  
 PT mammalian telomerase.  
 XX  
 PS Example 1; Col 27-28; 45pp; English.

CC The present sequence represents a peptide nucleic acid molecule which  
 CC hybridises to the mRNA component of mammalian telomerase, and inhibits  
 CC telomerase activity. Telomerase is a ribonucleoprotein enzyme that  
 CC synthesizes one strand of the telomeric DNA, using as a template an 11  
 CC nucleotide sequence contained within the RNA component of the enzyme. The  
 CC invention relates to PNA molecules having a sequence of no more than 25  
 CC bases, which include the sequence GTTAGG. The uncharged nature of the PNA  
 CC backbone increases the melting temperature of associating strands,  
 CC increases the rate of association with targeted nucleic acids, and  
 CC affords greater resistance of degradation by proteases or nucleases. The  
 CC therapeutic PNAs may be used for treating disease conditions such as  
 CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human  
 CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency  
 CC syndrome) and associated pathologies, fungal infections, and other  
 CC diseases characterized by abnormal telomere metabolism or telomerase  
 CC activity, in combination with antineoplastic and other cytotoxic or  
 CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be  
 CC used for molecular diagnostics, labelled PNAs are used as hybridization  
 CC probes to detect or quantitate polynucleotides having a human telomerase  
 CC RNA (htr) sequence. PNA probes are also used for forensic identification  
 CC of individuals, e.g. paternity testing, based on htr gene restriction  
 CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as  
 CC probes to detect the RNA component of a mammalian telomerase and as  
 CC inhibitors of telomerase activity. The method of the present invention  
 CC allows cancerous conditions to be detected with increased confidence and  
 CC possibly at an earlier stage, before cells are detected as cancerous  
 CC based on pathological characteristics. The diagnostic and prognostic  
 CC methods of the present invention can be used to detect an immortal or  
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the  
 CC cell expresses telomerase activity and its RNA component

Query Match 2.0%; Score 12; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330  
 |||||  
 Db 1 AGGATCTTCACC 12

RESULT 261  
 AA277376/c  
 ID AA277376 standard; DNA; 20 BP.

AC AA277376;

DT 10-SEP-2001 (first entry)

DE Human biallelic marker downstream amplification primer SEQ ID NO:11732.

KM Human genome; biallelic marker; high density disequilibrium map;  
 KM genomic map; haplotype; phenotype; polymorphic bases; genotyping;  
 KM haplotyping; hybridisation; identification; characterization;  
 KM amplification; single nucleotide polymorphism; SNP; PCR primer;  
 KM diagnosis; ss.

OS Homo sapiens.

XX WO9954500-A2.  
 PN 28-OCT-1999.  
 PD 21-APR-1999; 99WO-IB000822.  
 XX 21-APR-1998; 98US-0082614P.  
 PR 23-NOV-1998; 98US-0109732P.  
 XX (GEST ) GENSET.  
 PA Cohen D, Blumenfeld M, Chumakov I;  
 PI WPI; 2000-013267/01.  
 DR Novel biallelic markers used to construct a high density disequilibrium  
 PT map of the human genome.  
 PS Claim 9; Page 2731; 2745pp; English.  
 XX AA265654 to AA269578 represent human biallelic markers from the present  
 CC invention, which contain a polymorphic base at position 24 of their  
 CC nucleotide sequences. AA269579 to AA277440 represent amplification  
 CC primers for the biallelic markers. The biallelic markers of the invention  
 CC have a variety of uses: they can be used for high density mapping of the  
 CC human genome, and in complex association studies and haplotyping studies  
 CC which are useful in determining the genetic basis for disease states.  
 CC Compositions and methods of the invention can also be useful for the  
 CC identification of the targets for the development of pharmaceutical  
 CC agents and diagnostic methods, as well as the characterisation of the  
 CC differential efficacious responses to and side effects from  
 CC pharmaceutical agents acting on a disease as well as other treatment.  
 CC N.B. The SEQ ID NOS 2852, 2813, 2974, 3035, 3086, 3157, 3227, 3297 and  
 CC 3367, are not actually given a sequence in the Sequence Listing from the  
 CC present invention  
 CC  
 SQ Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 511 CGTCTCTCCAGA 522  
 Db 14 CGTCTCTCCAGA 3  
 RESULT 262  
 AA247037  
 ID AA247037 standard; DNA; 20 BP.  
 XX  
 AC AA247037;  
 XX  
 DT 15-MAR-2000 (first entry)  
 XX  
 DE Primer #2 for human beta-actin gene.  
 XX  
 KW Antiviral; anticancer; antiproliferative; human; interferon-alphas;  
 KW hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;  
 KW liver; gene expression; primer; PCR; amplification; beta-actin; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN WO9958143-A1.  
 XX  
 PD 18-NOV-1999.  
 XX  
 PF 13-MAY-1999; 99WO-ES000134.  
 XX  
 PR 13-MAY-1998; 98US-00001003.  
 XX

PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX Prieto Valtuena J, Civeira Murillo MP, Larrea Leoz E;  
 XX WPI; 2000-038959/03.  
 XX  
 DR Treating liver diseases with interferon-alphas or nucleic acid encoding  
 PT it, particularly chronic hepatitis C.  
 XX  
 PS Disclosure; Page 11; 36pp; Spanish.  
 XX  
 CC The invention relates to a method of using interferon-alphas or its  
 CC coding sequence to prepare compositions for treatment of hepatic  
 CC diseases, e.g. (i) chronic hepatitis C; (ii) cirrhosis of viral origin  
 CC and (iii) hepatocellular carcinoma. The method restores the level of  
 CC interferon-alphas, which is reduced in diseased liver cells, to normal  
 CC levels. The primers AA247036-247037 were used initially to detect the  
 CC level of expression of beta-actin gene in liver tissue by PCR as a  
 CC control for detecting the level of interferon-alpha or beta. The primers  
 CC amplify a 314 bp fragment of the human beta-actin gene  
 CC  
 SQ Sequence 20 BP; 4 A; 2 C; 8 G; 6 T; 0 U; 0 Other;  
 Query Match 2.0%; Score 12; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 317 TGAGATCTTCA 328  
 Db 3 TGAGATCTTCA 14  
 RESULT 263  
 AA66151/C  
 ID AA66151 standard; DNA; 20 BP.  
 XX  
 AC AA66151;  
 XX  
 DT 09-OCT-2000 (first entry)  
 XX  
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:13.  
 XX  
 KW Dog; genome; genomic marker; radiation hybrid map; identification;  
 KW chromosome location; gene marker; polymorphic microsatellite marker;  
 KW phenotype; behaviour; pedigree; ss.  
 XX  
 OS Canis familiaris.  
 XX  
 PN WO200029615-A2.  
 XX  
 PD 25-MAY-2000.  
 XX  
 PF 15-NOV-1999; 99WO-IB001907.  
 XX  
 PR 13-NOV-1998; 98US-0108193P.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Gallibert F, Andre C;  
 XX  
 DR WPI; 2000-387821/33.  
 XX  
 XX New radiation hybrid map of the dog, Canine familiaris, genome, useful  
 PT for e.g. identifying genes implicated in phenotypic and behavioral traits  
 PT or in genetic diseases and for studying dog pedigrees.  
 XX  
 PS Claim 1; Page 53; 87pp; English.  
 XX  
 CC The present invention describes a radiation hybrid map of the dog (Canine  
 CC familiaris) genome comprising the genome location of a marker selected  
 CC from AA66139 to AA66942. The radiation hybrid map is useful for  
 CC identifying and localising dog genes, since it covers approximately 80 %  
 CC of the dog genome and provides a dense map integrating different types



```

KM immunosuppressive; phosphorothioate; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /label= OTHER
FT /note= "phosphorothioate internucleotide linkages"
XX US6294650-B1.
XX 25-SEP-2001.
XX 08-JUL-1999; 99US-00349532.
XX 09-APR-1996; 96US-00630019.
XX 09-APR-1997; 97US-00838545.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Shay JW, Wright WE, Piatyzek MA, Corey DR, Norton JC,
XX WPI; 2001-638024/73.
XX
XX New peptide nucleic acid that hybridizes to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases.
XX
XX Example 1; Col 29; 46bp; English.
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridizing to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component of
XX mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase RNA
XX component (hTR) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the hTR gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents a phosphorothioate (PS)
XX oligomer used to inhibit telomerase activity in the methods of the
XX present invention.
XX
XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 4; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 319 AGGATCTCACC 330
XX |||||
XX 1 AGGATCTCACC 12
XX
XX RESULT 267
XX ID AAS15455 standard; DNA; 20 BP.
XX AC AAS15455;
XX XX
XX DT 14-FEB-2002 (first entry)
XX XX
XX DE PNA XIV inhibiting human and mammalian telomerase activity.

```

```

XX KM Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
XX KM human telomerase RNA component; hTR gene RFLP pattern; cancer;
XX KM inflammation; lymphoproliferative disease; autoimmune disease;
XX KM neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
XX KM human immunodeficiency virus; acquired immunodeficiency syndrome;
XX KM telomere metabolism; mutant; cytostatic; anti-inflammatory;
XX KM immunosuppressive; polyamide backbone; ss.
XX Homo sapiens.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /note= "this sequence is a peptide nucleic acid, i.e. it
FT contains a polyamide backbone instead of a deoxyribose
FT backbone"
XX US6294650-B1.
XX 25-SEP-2001.
XX 08-JUL-1999; 99US-00349532.
XX 09-APR-1996; 96US-00630019.
XX 09-APR-1997; 97US-00838545.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Shay JW, Wright WE, Piatyzek MA, Corey DR, Norton JC,
XX WPI; 2001-638024/73.
XX
XX New peptide nucleic acid that hybridizes to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases.
XX
XX Example 1; Col 29; 46bp; English.
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridizing to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component of
XX mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase RNA
XX component (hTR) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the hTR gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents one of the PNA sequences of the
XX present invention.
XX
XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 4; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 319 AGGATCTCACC 330
XX |||||
XX 1 AGGATCTCACC 12
XX
XX RESULT 268
XX ID AAT75831
XX

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